



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 169483**

**TO: David Lukton**  
**Location: rem/3B75/3C18**  
**Art Unit: 1654**

*Oct 26*, 2005

**Case Serial Number: 10/014147**

**From: P. Sheppard**  
**Location: Remsen Building**  
**Phone: (571) 272-2529**

**sheppard@uspto.gov**

### **Search Notes**

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ACCESS DB # 169483  
PLEASE PRINT CLEARLY

SEARCH REQUEST FORM  
(STIC)

10/25/05 ME

Requestor's Name: David Lukton Examiner number: 71263 Date:

10-014147

Art Unit: 1654 Phone number: 571-272-0952 Serial Number:

Mail Box: 3-C-18 Examiner Rm: 3-B-75 Results format: paper

\*\*\*\*\*

Title: SYNTHETIC PEPTIDES THAT INHIBIT LEUKOCYTE SUPEROXIDE ANION  
PRODUCTION AND/OR ATTRACT LEUKOCYTES

Applicants: BLECHA, FRANK; SHI, JISHU

Earliest Priority Date: 4/10/95

\*\*\*\*\*

Please search SEQ ID NOS: 1, 2, 5, 6, and 7

RECEIVED  
OCT 25 2005  
TECH/CHEM DIVISION  
(STIC)

\*\*\*\*\*

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: \_\_\_\_\_

\_\_\_\_ NA Sequence (#)

\_\_\_\_ STN \_\_\_\_\_ Dialog

Searcher Phone #: \_\_\_\_\_

\_\_\_\_ AA Sequence (#)

\_\_\_\_ Questel/Orbit \_\_\_\_\_ Lexis/Nexis

Searcher Location: \_\_\_\_\_

\_\_\_\_ Structure (#)

\_\_\_\_ Westlaw \_\_\_\_\_ WWW/Internet

Date Searcher Picked Up: \_\_\_\_\_

\_\_\_\_ Bibliographic

\_\_\_\_ In-house sequence systems

Date Completed: \_\_\_\_\_

\_\_\_\_ Litigation

\_\_\_\_ Commercial \_\_\_\_\_ Oligomer \_\_\_\_\_ Score/Length  
\_\_\_\_ Interference \_\_\_\_\_ SPDI \_\_\_\_\_ Encode/Transl  
\_\_\_\_ Other (specify)

Searcher Prep & Review Time: \_\_\_\_\_

\_\_\_\_ Fulltext

Online Time: \_\_\_\_\_

\_\_\_\_ Other

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:51:43 ; Search time 153.518 Seconds  
(without alignments)  
98.253 Million cell updates/sec

Title: US-10-014-147-1  
Perfect score: 238  
Sequence: 1 RRRPRPPVLP RPPPPPPPPRLLP RPPPPPPRFP 39

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %		Match	Length	DB	ID	Description
	Score	Match					
1	238	100.0	39	2	AAR30491	Aar30491	Antibacte
2	238	100.0	39	2	AAR99121	Aar99121	Magainin-
3	238	100.0	39	2	AAR94446	Aar94446	Synducin
4	238	100.0	39	2	AAW01446	Aaw01446	Leukocyte
5	238	100.0	39	2	AAW75722	Aaw75722	Proline/A
6	238	100.0	39	3	AAB26888	Aab26888	PR-39 pep
7	238	100.0	39	4	AAB97280	Aab97280	PR-39 pep
8	238	100.0	39	4	AAB84690	Aab84690	Amino aci
9	238	100.0	39	8	ADD35364	Add35364	Antimicro
10	238	100.0	39	8	ADE86112	Ade86112	Proline-a
11	238	100.0	39	8	ADL67254	Adl67254	Antimicro
12	238	100.0	42	5	ABB07714	Abb07714	Antimicro
13	238	100.0	42	8	ADR82250	Adr82250	Cell perm
14	238	100.0	44	4	AAB51194	Aab51194	E. coli A
15	155	65.1	26	2	AAW01447	Aaw01447	Leukocyte
16	155	65.1	26	2	AAW75723	Aaw75723	Proline/A
17	155	65.1	26	8	ADE86113	Ade86113	Proline-a
18	155	65.1	26	8	ADL67255	Adl67255	Antimicro
19	140	58.8	23	2	AAW01451	Aaw01451	Leukocyte
20	140	58.8	23	8	ADE86114	Ade86114	Proline-a
21	140	58.8	23	8	ADL67256	Adl67256	Antimicro
22	116	48.7	19	2	AAW01452	Aaw01452	Leukocyte
23	116	48.7	19	8	ADE86115	Ade86115	Proline-a
24	116	48.7	19	8	ADL67257	Adl67257	Antimicro
25	105	44.1	87	8	ABO57093	Abo57093	Human gen

26	102.5	43.1	205	6	ABU20105	Abu20105	Protein e
27	102.5	43.1	763	3	AAG38942	Aag38942	Arabidops
28	101.5	42.6	250	3	AAY67470	Aay67470	Np70 prot
29	101.5	42.6	311	2	AAV17387	Aay17387	Human DNA
30	101.5	42.6	389	7	ADE59849	Ade59849	Rat Prote
31	101.5	42.6	502	4	ABB66956	Abb66956	Drosophil
32	101.5	42.6	641	3	AAV67469	Aay67469	Np70 prot
33	101.5	42.6	641	3	AAV82327	Aay82327	Human Npw
34	101.5	42.6	641	4	AAV72165	Aay72165	Human RNA
35	101.5	42.6	641	4	AAB47514	Aab47514	NpwBP. 12
36	101.5	42.6	641	6	ABO53032	Abo53032	Human put
37	101.5	42.6	641	7	ADE59851	Ade59851	Human Pro
38	101.5	42.6	647	3	AAB53462	Aab53462	Human col
39	101	42.4	79	2	AAR82569	Aar82569	Pig leuko
40	101	42.4	79	2	AAR82562	Aar82562	Pig leuko
41	101	42.4	79	2	AAR82566	Aar82566	Pig leuko
42	101	42.4	79	2	AAR82564	Aar82564	Pig leuko
43	100.5	42.2	649	7	ADC87385	Adc87385	Human GPC
44	99	41.6	143	4	AAU56017	Aau56017	Propionib
45	99	41.6	143	6	ABM52536	Abm52536	Propionib

ALIGNMENTS

RESULT 1  
AAR30491  
ID AAR30491 standard; peptide; 39 AA.

XX AC AAR30491;

XX XX  
DT 25-MAR-2003 (revised)  
DT 12-MAY-1993 (first entry)

XX DE Antibacterial peptide.

XX KW Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;  
KW veterinary medicine; prophylactic.

XX OS Sus scrofa domestica.

XX PN W09222578-A1.

XX PD 23-DEC-1992.

XX PF 10-JUN-1992; 92WO-SE000394.

XX PR 14-JUN-1991; 91SE-00001838.

XX PA (LEEJ/) LEE J.

XX PA (BOMA/) BOMAN H G.

XX PA (MUTT/) MUTT V.

XX PA (JOER/) JOERNVALL H.

XX PI Lee J, Boman HG, Mutt V, Joernvall H;

XX DR WPI; 1993-018080/02.

XX PT New anti-bacterial polypeptide - active against Gram negative bacteria.

XX PS Claim 1; Page 10; 15pp; English.

XX CC This peptide was isolated from the small intestine of a pig. The small  
XX CC intestine is an important endocrine organ and many physiologically active  
XX CC peptides have been isolated from it. This peptide inhibits the growth of,  
XX CC and may kill, bacteria, pref. gram negative bacteria. This peptide or its  
XX CC functional derivatives may be used in human or veterinary medicine for  
XX CC therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN  
XX CC field.)

XX SQ Sequence 39 AA;

Query Match 100.0%; Score 238; DB 2; Length 39;



OS Synthetic.  
XX WO9632129-A1.  
PN  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-US004674.  
XX  
PR 10-APR-1995; 95US-00419066.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
PI Blecha F, Shi J;  
XX WPI; 1996-476842/47.  
DR  
XX Inhibition of leukocyte super:oxide anion prodn. and attraction of  
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.  
PT  
XX Claim 2; Page 26; 45pp; English.  
PS  
XX This sequence represents the proline-arginine rich antimicrobial peptide  
CC PR39. The PR39 sequence was first isolated from porcine small intestine,  
CC and has also been identified in human and porcine neutrophils. PR39 kills  
CC bacteria by interfering with DNA and/or protein synthesis. PR39 also  
CC induces syndecan expression on mesenchymal cells. Syndecans are important  
CC in wound repair, showing that PR39 can be used in wound repair, as well  
CC as in antibacterial agents. This sequence, and the fragments of it shown  
CC in AAW01447-W01454, can be used in the method of the invention. The  
CC method of the invention is for inhibiting leukocyte superoxide anion (O2-  
CC ) production. The method comprises administering to a leukocyte a peptide  
CC (such as this sequence) capable of inhibiting leukocyte O2- production.  
CC The peptides can be used as medicaments for fighting infection by  
CC attracting leukocytes to a wound site and restricting tissue damage at  
CC the wound site caused by excessive oxygen radicals produced by these  
CC leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states  
XX  
SQ Sequence 39 AA;  
Query Match 100.0%; Score 238; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRRPPPPFPRLPPRIPPGFPFRFP 39  
DB 1 RRRPRPPYLP RRRPPPPFPRLPPRIPPGFPFRFP 39  
RESULT 5  
AAW75722  
ID AAW75722 standard; peptide; 39 AA.  
XX  
AC AAW75722;  
DT 19-NOV-1998 (first entry)  
XX  
DE Proline/Arginine rich peptide PR-39.  
XX  
KW Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;  
KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;  
KW coronary bypass; organ transplantation surgery.  
XX  
OS Synthetic.  
XX  
PN WO9835690-A1.  
XX  
PD 20-AUG-1998.  
XX  
PF 17-FEB-1998; 98WO-US003207.  
XX  
PR 18-FEB-1997; 97US-00802306.  
PR 16-FEB-1998; 98US-00024975.

XX (UNIV ) UNIV KANSAS STATE RES FOUND.  
PA  
XX Ross CR, Blecha F, Shi J;  
PI  
XX WPI; 1998-495359/42.  
DR  
XX Reduction of reperfusion injury in temporarily occluded blood vessels -  
PT by administration of a peptide which is rich in proline or arginine  
PT residues.  
XX  
PS Claim 3; Page 14; 35pp; English.  
XX  
CC Sequences AAW75722-W75732 are proline/arginine rich peptides that upon  
CC administration into a mammal's bloodstream reduce reperfusion injury  
CC (production of reactive oxygen species, neutrophil adherence to  
CC endothelium, and extravasation of neutrophils). These peptides have two  
CC requirements: they contain the consensus sequence PXXP, where P is a  
CC proline residue and X is any amino acid residue, which has been found to  
CC inhibit superoxide production, and secondly they have arginine residues  
CC adjacent to these motifs, required for effective inhibition. It was  
CC established by structural and function analysis that a peptide should  
CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is  
CC correlated with the increase of length of peptides. The effectiveness of  
CC these peptides was determined by investigating the production of the  
CC neutrophil superoxide anion, and also the inhibition of neutrophil  
CC chemotaxis. From this, it was found that all of the peptides inhibited  
CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil  
CC oxidase activity. PR-39 is believed, to be the most potent endogenous  
CC down regulator of NADPH oxidase yet discovered, and from the data  
CC produced, it can be suggested to be involved in eliminating or reducing  
CC the reperfusion injury induced adhesion and extraction of neutrophils.  
CC The peptides are also useful in connection with surgical procedures such  
CC as coronary bypass and organ transplantation surgery  
XX  
SQ Sequence 39 AA;  
Query Match 100.0%; Score 238; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRRPPPPFPRLPPRIPPGFPFRFP 39  
DB 1 RRRPRPPYLP RRRPPPPFPRLPPRIPPGFPFRFP 39  
RESULT 6  
AAB26888  
ID AAB26888 standard; peptide; 39 AA.  
XX  
AC AAB26888;  
XX  
DT 01-FEB-2001 (first entry)  
XX  
DE PR-39 peptide used in angiogenesis control.  
XX  
KW Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;  
KW myocardial ischaemia; proteasome.  
XX  
OS Synthetic.  
XX  
PN WO200057895-A1.  
XX  
PD 05-OCT-2000.  
XX  
PF 16-MAR-2000; 2000WO-US007050.  
XX  
PR 26-MAR-1999; 99US-00276868.  
XX  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Simons M, Gao Y;  
XX

DR WPI; 2000-628319/60.

XX Stimulating angiogenesis in situ, useful e.g. for treating anoxia and

PT infarction, by administering a PR-39 oligopeptide that regulates

PT enzymatic activity of proteasomes.

XX Disclosure; Page 21; 51pp; English.

XX This invention relates to a method for the stimulation of angiogenesis in

CC situ within a targeted collection of viable cells. The method comprises

CC introducing, into the cytoplasm, at least 1 member of the PR-39

CC oligopeptide collective, which interacts with cytoplasmic proteasomes.

CC Part of the proteolytic activity of the proteasomes is selectively

CC altered so as to stimulate angiogenesis. The method is used to induce

CC angiogenesis in tissue that has suffered anoxia or infarction, e.g.

CC myocardial infarction or chronic myocardial ischaemia, and also to study

CC the mechanisms that control angiogenesis. The present sequence represents

CC the PR-39 peptide from which peptide used in the method of the invention

CC are derived

XX Sequence 39 AA;

SQ Query Match 100.0%; Score 238; DB 3; Length 39;

Best Local Similarity 100.0%; Pred. No. 2.7e-15;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRPPPYLPRPRPPPPFFPPRLPPRIPPGFPPRPPRFP 39

Db 1 RRRRPPPYLPRPRPPPPFFPPRLPPRIPPGFPPRPPRFP 39

RESULT 7

AAB97280

ID AAB97280 standard; peptide; 39 AA.

XX AAB97280;

XX 09-AUG-2001 (first entry)

XX PR-39 peptide.

XX PR-39; cathelin; inflammation; wound healing; myocardial infarction;

KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;

KW anoxia; chronic myocardial ischaemia; heart tissue.

XX Unidentified.

OS WO200130368-A1.

PN 03-MAY-2001.

XX 06-OCT-2000; 2000WO-US027552.

PF 25-OCT-1999; 99US-00426011.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Simons M, Gao Y;

XX WPI; 2001-355179/37.

XX Stimulation of angiogenesis and inhibition of proteasome mediated

PT degradation in cells, by introduction of PR-39 oligopeptide or its N-

PT terminal fragments or their conjugates, for use in anoxia and infarction

PT conditions.

XX Disclosure; Page 21; 52pp; English.

XX Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39

CC is a member of the cathelin family of proteins, mature PR-39

CC represented by the present sequence is 39 amino acids in length, and has

CC been shown to play a role in several inflammatory events including wound

CC healing and myocardial infarction. The PR-39 derived family of

CC oligopeptides cause selective inhibition of proteasome mediated

CC degeneration of peptides and stimulation of angiogenesis after their

CC intracellular introduction to a target cell. PR-39 derived peptides are

CC able to interact with at least the alpha7 subunit of the proteasomes, and

CC therefore alter the proteolytic activity of proteasomes such that a

CC selective increased expression of specific proteins occurs. The invention

CC includes methods for the selective inhibition of proteasome mediated

CC peptide degradation. The method provides means for stimulating

CC angiogenesis as required in living tissues and organs which have suffered

CC defects or have undergone anoxia and/or infarction, myocardial infarction

CC or chronic myocardial ischaemia of heart tissue. Examples are the

CC myocardium, skeletal or smooth muscle, artery or vein, lung, brain,

CC kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and

CC extremities. A particular example is after myocardial infarction or

CC ischaemia

XX Sequence 39 AA;

SQ Query Match 100.0%; Score 238; DB 4; Length 39;

Best Local Similarity 100.0%; Pred. No. 2.7e-15;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRPPPYLPRPRPPPPFFPPRLPPRIPPGFPPRPPRFP 39

Db 1 RRRRPPPYLPRPRPPPPFFPPRLPPRIPPGFPPRPPRFP 39

RESULT 8

AAB84690

ID AAB84690 standard; protein; 39 AA.

XX AAB84690;

XX 17-SEP-2001 (first entry)

DE Amino acid sequence of a PR-39 protein.

XX PR-39; IkappaBalpa degradation; NfkappaB transcription factor;

KW myocardial infarction; chronic myocardial ischemia; heart disease;

KW anoxia.

XX Unidentified.

OS WO200147540-A1.

PN 05-JUL-2001.

PD 27-DEC-2000; 2000WO-US035293.

XX 29-DEC-1999; 99US-00474967.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Simons M, Gao Y;

XX WPI; 2001-441690/47.

XX Selective inhibition of IkappaBalpa degradation within targeted viable

PT cell collection, involves interacting PR-39 oligopeptide with

PT IkappaBalpa and proteasomes, and altering proteolytic activity of

PT proteasomes.

XX Disclosure; Page 30; 69pp; English.

XX The present sequence represents a PR-39 protein. The specification

CC describes PR-39 derived peptides, which are used for selective inhibition

CC of IkappaBalpa degradation within a targeted cell collection in-situ.

CC The method is useful for selectively inhibiting IkappaBalpa protein

CC degradation in situ, decreasing the activity of NfkappaB transcrption

CC factor and selective control of NfkappaB-dependent gene expression in

CC situ. The PR-39 derived peptides are useful in the treatment of

CC myocardial infarction, chronic myocardial ischemia of heart disease and

CC anoxia



XX SQ Sequence 39 AA;

Query Match 100.0%; Score 238; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPPPPFFPPRLPPRIIPGPPPPRPPRFP 39  
Db 1 RRRPRPPYLPRPPPPFFPPRLPPRIIPGPPPPRPPRFP 39

RESULT 9  
ADD35364  
ID ADD35364 standard; peptide; 39 AA.  
XX  
AC ADD35364;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39.  
XX  
KW antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological;  
KW intraocular pressure; glaucoma; ocular hypertension; hyperaemia;  
KW irritation; inflammation; conjunctiva; ocular cell dysplasia;  
KW iridial melanocyte hyperplasia; hyperpigmentation.  
XX  
OS Unidentified.  
XX  
PN WO2003079997-A2.  
XX  
PD 02-OCT-2003.  
XX  
PF 21-MAR-2003; 2003WO-US008935.  
XX  
PR 21-MAR-2002; 2002US-0367071P.  
XX  
PA (CAYM-) CAYMAN CHEM CO.  
XX  
PI Maxey KM, Johnson J;  
XX  
DR WPI; 2004-011506/01.  
XX  
PT Ophthalmic solution useful for the treatment of increased intraocular  
PT pressure comprises a prostaglandin of the F-series and an antimicrobial  
PT peptide.  
XX  
PS Disclosure; Page 11; 11pp; English.  
XX  
CC The invention relates to a novel ophthalmic solution comprising a  
CC prostaglandin of the F-series and an antimicrobial peptide. A solution of  
CC the invention has hypotensive and ophthalmological activity. The solution  
CC is useful for the treatment of increased intraocular pressure, such as  
CC caused by glaucoma and for the reduction of ocular hypertension. The  
CC prostaglandin and the antimicrobial peptide work synergistically, to  
CC provide beneficial reduction in the incidence of irritant and toxic side  
CC effects such as hyperaemia, irritation and inflammation of conjunctiva,  
CC ocular cell dysplasia, iridial melanocyte hyperplasia, and  
CC hyperpigmentation, associated with the prior art prostaglandin  
CC compositions. The present sequence represents an antimicrobial peptide of  
CC the invention.  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 238; DB 8; Length 39;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPPPPFFPPRLPPRIIPGPPPPRPPRFP 39  
Db 1 RRRPRPPYLPRPPPPFFPPRLPPRIIPGPPPPRPPRFP 39

RESULT 10  
ADE86112  
ID ADE86112 standard; peptide; 39 AA.  
XX  
AC ADE86112;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Proline-arginine (PR)-rich antimicrobial peptide PR-39.  
XX  
KW Leukocyte superoxide anion; leukocyte O2- production;  
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;  
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;  
KW tissue damage; oxygen radical; antibacterial.  
XX  
OS Synthetic.  
XX  
PN US2003125249-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 07-DEC-2001; 2001US-00014147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 2004-059188/06.  
XX  
PT Attracting leukocyte to location by administering peptide including  
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to  
PT the location.  
XX  
PS Claim 2; SEQ ID NO 1; 24pp; English.  
XX  
CC The present invention relates to a method of inhibiting leukocyte  
CC superoxide anion (O2-) production and/or attracting leukocytes. The  
CC method comprises the use of proline-arginine (PR)-rich antimicrobial  
CC peptides or their truncated analogues. The method is useful for  
CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or  
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are  
CC useful as medicaments to fight infection by attracting leukocytes to a  
CC wound site, while restricting tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leukocytes. The present  
CC sequence represents a PR-rich antimicrobial peptide.  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 238; DB 8; Length 39;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPPPPFFPPRLPPRIIPGPPPPRPPRFP 39  
Db 1 RRRPRPPYLPRPPPPFFPPRLPPRIIPGPPPPRPPRFP 39

RESULT 11  
ADL67254  
ID ADL67254 standard; peptide; 39 AA.  
XX  
AC ADL67254;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39.  
XX  
KW Leucocyte ; superoxide anion; oxygen radical; proline-arginine ;  
KW antimicrobial; antioxidant; NADPH oxidase ; p47phox; neutrophil;



KW cytostatic; anticonvulsant; nootropic; muscular; anti-HIV;  
KW RNA interference; iRNA; antisense technology; lipid metabolism;  
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
KW coronary artery disease; CAD; coronary heart disease; CHD;  
KW atherosclerosis; hepatic glucose production;  
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
KW colon cancer; lung cancer; neurological disease; Huntington disease;  
KW spinocerebellar ataxia; viral disease; AIDS; cell permeation peptide;  
KW bactenecin.  
XX Unidentified.  
XX WO2004080406-A2.  
PN 23-SEP-2004.  
XX 08-MAR-2004; 2004WO-US007070.  
XX 07-MAR-2003; 2003US-0452682P.  
PR 12-MAR-2003; 2003US-0454265P.  
PR 13-MAR-2003; 2003US-0454962P.  
PR 13-MAR-2003; 2003US-0455050P.  
PR 14-APR-2003; 2003US-0462894P.  
PR 17-APR-2003; 2003US-0463772P.  
PR 25-APR-2003; 2003US-0465665P.  
PR 25-APR-2003; 2003US-0465802P.  
PR 09-MAY-2003; 2003US-0469612P.  
PR 08-AUG-2003; 2003US-0493986P.  
PR 11-AUG-2003; 2003US-0494597P.  
PR 26-SEP-2003; 2003US-0506341P.  
PR 09-OCT-2003; 2003US-0510246P.  
PR 10-OCT-2003; 2003US-0510318P.  
PR 07-NOV-2003; 2003US-0518453P.  
XX (ALNY-) ALNYLAM PHARM.  
PA Manoharan M, Bumcrot D;  
XX WPI; 2004-677362/66.  
XX Interference RNA agent useful for treating dyslipidemias, coronary artery  
PT disease, diabetes, cancer or neurological disease, comprises sense  
PT sequence and antisense sequence which has specific modifications.  
XX Disclosure; SEQ ID NO 6749; 378pp; English.  
PS The invention describes a RNA interference (iRNA) agent (I) comprising a  
XX sense sequence and an antisense sequence, where the sense sequences have  
CC one or more asymmetrical 2'-O alkyl modifications, the antisense  
CC sequences have one or more asymmetrical phosphorothioate modifications  
CC and the antisense sequence targets a human gene sequence. Also described  
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100  
CC levels or glucose-6-phosphatase levels in a subject; producing (I);  
CC stabilising (I), involves selecting a sequence with activity and  
CC introducing one or more asymmetrical modification in the sequence, where  
CC the modification decreases nuclease sensitivity while not decreasing its  
CC activity; a kit comprising (I) and instruction for its use; and a device  
CC that can be dispense or administer a composition comprising (I). (I) is  
CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)  
CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.  
CC The subject is suffering from a disorder characterised by elevated or  
CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted  
CC levels of cholesterol, and/or dysregulation of lipid metabolism. The  
CC disorder is chosen from the HDL/LDL cholesterol imbalance,  
CC dyslipidaemias, hypercholesterolaemia, statin-resistant  
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
CC inhibit hepatic glucose production or for treating glucose-metabolism-  
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
CC lung cancer), neurological disease (e.g., Huntington disease or  
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This is the amino  
CC acid sequence of a cell permeation peptide that can be used as a ligand

CC to increase the uptake of iRNA's.  
XX Sequence 42 AA;  
SQ Query Match 100.0%; Score 238; DB 8; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.9e-15;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RRRPRPPYLPRPRPPPPFFPPRLPPRIPPPGPPRFRFP 39  
Db 1 RRRPRPPYLPRPRPPPPFFPPRLPPRIPPPGPPRFRFP 39  
RESULT 14  
AAB51194  
ID AAB51194 standard; peptide; 44 AA.  
XX AAB51194;  
AC 22-MAR-2001 (first entry)  
XX E. coli AMP gene PR39 amino acid sequence.  
DE Escherichia coli; E. coli; AMP gene; anti-microbial peptide; screening;  
XX preservation; food; feed; paint formulation; detergent; cosmetic;  
KW medical device; prosthetic implant; disinfectant; microbial infection;  
KW tumour.  
XX Escherichia coli.  
OS WO200073433-A1.  
XX 07-DEC-2000.  
PD 29-MAY-2000; 2000WO-DK000287.  
XX 31-MAY-1999; 99DK-00000766.  
PR (NOVO ) NOVO NORDISK AS.  
XX Kristensen H;  
PI WPI; 2001-070965/08.  
XX Screening for nucleotide sequences encoding antimicrobial peptides by  
PT generating peptide libraries in microorganisms, inducing expression of  
PT peptides, selecting cells and recovering nucleotide sequences from cells.  
XX Example 1; Page 34; 59pp; English.  
PS The present invention describes a plasmid which is ligated with a pool of  
CC nucleotide sequences (NT) linked to an inducible promoter, to express a  
CC peptide (P) (an enzyme or mature (P) of less than 100 amino acids  
CC optionally linked to a signal (P)), transformed into host cells and  
CC cultured in presence of an inducer to induce expression of the NT. A  
CC method of screening (I) a pool of nucleotide sequences to select a  
CC nucleotide sequence encoding a peptide, comprises: (a) ligating a plasmid  
CC with the pool of NT; (b) transforming host cells which are sensitive to  
CC the peptide with the ligated plasmids; (c) screening the transformed  
CC cells to select viable cells; (d) cultivating the viable cells in the  
CC presence of an inducer to induce expression of NT; (e) selecting cells  
CC according to the effect of the inducer on cell growth; and (f) recovering  
CC NT encoding the peptide from the selected cells. (I) is useful for  
CC screening a pool of nucleotide sequences to select a nucleotide sequence  
CC encoding a peptide which is an antimicrobial peptide or an antimicrobial  
CC enzyme active on bacteria and for finding and preparing a composition for  
CC treatment of human or animal. The antimicrobial peptide obtained using  
CC (I) may be employed in preservation of e.g. food/feed, paint  
CC formulations, detergents, cosmetics, medical devices such as prosthetic  
CC implants and also to disinfect and/or kill microbial cells on an object  
CC e.g. as a disinfectant for the treatment of biofilm. The peptides are  
CC useful for treating microbial infections and/or tumours. Peptides with  
CC improved bio-activity can be developed using (I). The peptides have no





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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 29.0727 Seconds  
(without alignments)  
129.071 Million cell updates/sec

Title: US-10-014-147-1  
Perfect score: 238  
Sequence: 1 RRRPRPPYLPRPPPPPPPPRLPPRIPPGPPPPPPRFP 39

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: Pir1:.\*  
2: Pir2:.\*  
3: Pir3:.\*  
4: Pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	238	100.0	172	2	S68232		antimicrobial prot
2	122.5	51.5	199	2	S14981		extensin class I (
3	109.5	46.0	212	2	S57330		cathelin-like anti
4	107	45.0	301	2	JQ1663		hybrid proline-ric
5	105.5	44.3	997	2	T28872		hypothetical prote
6	102.5	43.1	228	2	S40463		prophenin (PF-2) p
7	98.5	41.4	42	2	B36589		bactenecin 5 - bov
8	98	41.2	1006	2	G86292		hypothetical prote
9	97.5	41.0	134	2	D84672		hypothetical prote
10	95	39.9	439	2	S51939		chitinase (BC 3.2.
11	94.5	39.7	221	2	T07176		extensin homolog -
12	94.5	39.7	382	2	I39068		proline- arginine-
13	94	39.5	176	2	A45328		bactenecin 5 precu
14	93	39.1	59	2	A36589		bactenecin 7 - bov
15	92.5	38.9	148	2	S39206		proline-rich prote
16	92.5	38.9	547	2	C96828		unknown protein F1
17	92	38.7	494	2	B96534		hypothetical prote
18	92	38.7	1460	1	EDBEIF		immediate-early pr
19	91.5	38.4	1560	2	T42727		proliferation pote
20	91	38.2	134	2	JC5572		proline-rich prote
21	91	38.2	424	2	A54964		spliceosome-associ
22	90.5	38.0	388	2	JC5437		spliceosome-associ
23	90.5	38.0	574	2	T43556		Wiskott-Aldrich sy
24	90.5	38.0	574	2	T38819		wiskott-aldrich sy
25	90.5	38.0	948	2	A57640		retinoblastoma bin
26	90	37.8	329	2	T10064		cytokinin-induced
27	89	37.4	141	2	A34043		hypothetical proli
28	89	37.4	599	2	T10798		pherophorin-S - Vo
29	88.5	37.2	1958	2	B40505		hypothetical prote

30	88	37.0	485	2	A33647	sulfated surface g
31	87.5	36.8	1098	2	T08599	probable transcrip
32	87	36.6	196	2	B48232	cysteine-rich exte
33	87	36.6	381	2	S52985	cell wall protein
34	87	36.6	487	2	S42442	nuclear protein EB
35	87	36.6	1206	2	S24407	formin isoform IV
36	87	36.6	1468	2	S11515	formin - mouse
37	86.5	36.3	1268	2	T31420	C-terminal domain-
38	86	36.1	57	2	S10782	salivary protein P
39	86	36.1	79	1	FJHUSB	proline-rich pepti
40	86	36.1	322	2	S09779	hypothetical prote
41	86	36.1	367	1	OZZQMY	circumsporozoite p
42	86	36.1	415	1	A34170	acrosin (EC 3.4.21
43	86	36.1	431	2	S47538	acrosin (EC 3.4.21
44	86	36.1	449	2	D87682	OmpA family protei
45	86	36.1	620	2	S06733	hydroxyproline-ric

ALIGNMENTS

RESULT 1

S68232  
antimicrobial protein PR-39 precursor, cathelin-associated - pig  
N;Alternate names: myeloid antibacterial protein PR-39  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S68232; JN0899; I47138; S19563  
R;Zhao, C.; Ganz, T.; Lehrer, R.I.  
FEBS Lett. 376, 130-134, 1995  
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni  
A;Reference number: S68232; MUID:96105365; PMID:7498526  
A;Accession: S68232  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-172 <ZHA>  
A;Cross-references: UNIPROT:P80054; EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g116:  
A;Experimental source: leukocytes  
R;Storici, P.; Zanetti, M.  
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993  
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i  
A;Reference number: JN0899; MUID:94071853; PMID:8250863  
A;Accession: JN0899  
A;Molecule type: mRNA  
A;Residues: 1-20,'A',22-172 <STO>  
A;Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101  
A;Experimental source: bone marrow cells  
R;Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bome  
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995  
A;Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam  
A;Reference number: I47138; MUID:95350216; PMID:7624374  
A;Accession: I47138  
A;Status: preliminary; translated from GB/EMBL/DBU  
A;Molecule type: DNA  
A;Residues: 1-28,'T',30-89,'QR',92-116,'NDP',120-172 <GUD>  
A;Cross-references: EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PID:g1051298  
R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,  
Eur. J. Biochem. 202, 849-854, 1991  
A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of th  
A;Reference number: S19563; MUID:92111534; PMID:1765098  
A;Accession: S19563  
A;Molecule type: protein  
A;Residues: 131-169 <AGE>  
A;Experimental source: intestine  
C;Genetics:  
A;Gene: PR39  
A;Intons: 66/3; 102/3; 126/3  
C;Superfamily: cathelin; cystatin homology  
C;Keywords: amidated carboxyl end; antibacterial  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;22-129/Domain: cystatin homology <CYS>  
F;30-130/Domain: propeptide #status predicted <PRO>  
F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>



A;Cross-references: UNIPROT:P51525; EMBL:X75438; NID:G443812; PIDN:CAA53188.1; PID:G4438  
R;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarčič, B.; Berbic, S.; Turk, V  
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995  
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte  
A;Reference number: S57330; MUID:96042752; PMID:7576250  
A;Accession: S57331  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-228 <STR>  
R;Zhao, C.; Ganz, T.; Lehner, R.I.  
FEBS Lett. 376, 130-134, 1995  
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen  
A;Reference number: S68232; MUID:96105365; PMID:7498526  
A;Accession: S68233  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-228 <ZHA>  
A;Cross-references: EMBL:X89202; NID:g1165148; PIDN:CAA61488.1; PID:g1165149  
C;Genetics:  
A;Introns: 66/3; 102/3; 126/3  
C;Superfamily: cathelin; cystatin homology  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;22-129/Domain: cystatin homology <CYS>  
F;30-228/Product: prophenin (Pr-2) #status predicted <MAT>  
  
Query Match 43.1%; Score 102.5; DB 2; Length 228;  
Best Local Similarity 51.9%; Pred. No. 0.012;  
Matches 28; Conservative 1; Mismatches 6; Indels 19; Gaps 6;  
  
QY 2 RRPR-----PPYLPRR-PPFFP-PRLPRIIPGFP-PRFP-----PRFP 39  
Db 139 RRRLRRQAFAFPNVPGRFPNVPGRFP---PFNFGPRFPNFPNFGPRFP 189  
  
RESULT 7  
B36589  
bactenecin 5 - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 08-Dec-1995  
C;Accession: B36589  
R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.  
J. Biol. Chem. 265, 18871-18874, 1990  
A;Title: Amino acid sequences of two proline-rich bacterenecins. Antimicrobial peptides of  
A;Reference number: A36589; MUID:91035404; PMID:2229048  
A;Accession: B36589  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-42 <FRA>  
C;Superfamily: cathelin; cystatin homology  
  
Query Match 41.4%; Score 98.5; DB 2; Length 42;  
Best Local Similarity 52.4%; Pred. No. 0.006;  
Matches 22; Conservative 1; Mismatches 14; Indels 5; Gaps 1;  
  
QY 3 RRRPPYLRPRPPPPFPPRLPRIPRIPGFPFRFP-----RFP 39  
Db 1 RFRPPIRRPPIRPPFYPPFRPPIRPPIRPPIRPPIRPPFRPPPLRFP 42  
  
RESULT 8  
G86292  
hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: G86292  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: G86292  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1006 <STO>  
A;Cross-references: UNIPROT:Q9LMQ1; GB:AB005172; NID:G8927662; PIDN:AAF82153.1; GSPDB:GNK  
C;Genetics:  
A;Map position: 1  
  
Query Match 41.2%; Score 98; DB 2; Length 1006;  
Best Local Similarity 58.8%; Pred. No. 0.12;  
Matches 20; Conservative 1; Mismatches 11; Indels 2; Gaps 1;  
  
QY 4 PRPPYLPRPRPPPPFPPRLPRIPRIPGFPFRFP 37  
Db 99 PRPPRRPRPRP--SPRLPPLVPSPPPLHPR 130  
  
RESULT 9  
D84672  
hypothetical protein At2g27390 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: D84672  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: D84672  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-134 <STO>  
A;Cross-references: UNIPROT:Q9XIP3; GB:AE002093; NID:G5306259; PIDN:AAD41991.1; GSPDB:GNK  
C;Genetics:  
A;Gene: At2g27390  
A;Map position: 2  
  
Query Match 41.0%; Score 97.5; DB 2; Length 134;  
Best Local Similarity 53.8%; Pred. No. 0.021;  
Matches 21; Conservative 1; Mismatches 14; Indels 3; Gaps 2;  
  
QY 4 PRPPYLPR-PRPPFFPPRLPRIPPGF--PRFPFRFP 39  
Db 65 PEPPLPRFELPPLFPPLPPLRLPPLPPLPPPEPRFP 103  
  
RESULT 10  
S51939  
chitinase (EC 3.2.1.14) precursor - beet  
C;Species: Beta vulgaris (beet)  
C;Date: 28-Oct-1996 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: S51939; S72315; S45025  
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A.  
Plant Mol. Biol. 27, 211-216, 1995  
A;Title: A proline-rich chitinase from Beta vulgaris.  
A;Reference number: S51939; MUID:95170004; PMID:7865792  
A;Accession: S51939  
A;Molecule type: DNA  
A;Residues: 1-439 <BER>  
A;Cross-references: UNIPROT:Q42421; EMBL:X79301; NID:G488730; PID:G488731  
A;Note: the authors translated the codon TGC for residue 416 as Gly  
A;Accession: S72315  
A;Molecule type: mRNA  
A;Residues: 191-397 <BER2>  
C;Genetics:  
A;Introns: 248/1; 300/2  
C;Keywords: glycosidase; hydrolase  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-439/Product: chitinase #status predicted <MAT>



F:183-423/Domain: plant chitinase homology <PCH>

Query Match 39.9%; Score 95; DB 2; Length 439;  
Best Local Similarity 55.3%; Pred. No. 0.1;  
Matches 21; Conservative 0; Mismatches 15; Indels 2; Gaps 1;

QY 4 PRPPYLPRRPPPPFFP--PRLPPRIPPGGFPPRFPFRFP 39  
||||| | ||||| | ||||| | ||||| | ||||| |  
Db 122 PRPPPPPTPRPPPPSPPTPRPPPPPPPPSPPTSPSP 159

RESULT 11

T07176

extensin homolog - potato (fragment)  
C:Species: Solanum tuberosum (potato)  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T07176  
R:MacLeod, M.R.  
submitted to the EMBL Data Library, December 1997  
A:Reference number: Z15977  
A:Accession: T07176  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-221 <MAC>  
A:Cross-references: UNIPROT:O49946; EMBL:AJ003220; NID:e1251331; PIDN:CAA06000.1; PID:e1  
A:Experimental source: cv. Record; swelling stolon  
C:Superfamily: glutelin

Query Match 39.7%; Score 94.5; DB 2; Length 221;  
Best Local Similarity 56.4%; Pred. No. 0.061;  
Matches 22; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

QY 1 RRRRPPPYLPRRPPPPFFPPRLPPRIPPGGFPPRFPFRFP 39  
| | | | | | | | | | | | | | | | | | | | | |  
Db 40 RPYCPKPKRPSPPP-PPRSPPPPPPSPPP--PPPTP 75

RESULT 12

I39068

proline- arginine-rich end leucine-rich repeat protein PRELP precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C:Accession: I39068  
R:Bengtsson, E.; Neame, P.J.; Heinegard, D.; Sommarin, Y.  
J. Biol. Chem. 270, 25639-25644, 1995  
A:Title: The primary structure of a basic leucine-rich repeat protein, PRELP, found in c  
A:Reference number: I39068; MUID:96029653; PMID:7592739  
A:Accession: I39068  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-382 <RES>  
A:Cross-references: UNIPROT:P51888; EMBL:U29089; NID:g886135; PIDN:AAC50230.1; PID:g8861  
C:Genetics:  
A:Gene: GDB:PRELP  
A:Cross-references: GDB:696218  
A:Map position: 1q32.1-1q32.1  
C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology  
C:Keywords: tandem repeat

Query Match 39.7%; Score 94.5; DB 2; Length 382;  
Best Local Similarity 41.0%; Pred. No. 0.1;  
Matches 25; Conservative 1; Mismatches 12; Indels 23; Gaps 3;

QY 2 RRPRPPY-----LPRRPPPPFF-----PPRLPPRIPPGGFPPRF-----PPRF 38  
||||| | ||||| | | ||||| | | ||||| | | ||||| |  
Db 24 RRPRGTGGRRRPRRPRPTPSFPQPDEAEFTDLPPLPPGPPSIFPDCPRECYCPDF 83

QY 39 P 39  
|  
Db 84 P 84

RESULT 13

A45328

bactenecin 5 precursor - bovine  
N:Alternate names: Bac5; neutrophil antibiotic protein 5  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: A45328  
R:Zanetti, M.; Del Sal, G.; Storici, P.; Schneider, C.; Romeo, D.  
J. Biol. Chem. 268, 522-526, 1993  
A:Title: The cDNA of the neutrophil antibiotic Bac5 predicts a pro-sequence homologous to  
A:Reference number: A45328; MUID:93107055; PMID:8416958  
A:Accession: A45328  
A:Molecule type: mRNA  
A:Residues: 1-176 <ZAN>  
A:Cross-references: UNIPROT:P19660; GB:L02650; NID:g162730; PIDN:AAA30404.1; PID:g162731  
A>Note: sequence extracted from NCBI backbone (NCBIP:121443)  
C:Superfamily: cathelin; cystatin homology  
C:Keywords: amidated carboxyl end; antibacterial  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:22-129/Domain: cystatin homology <CYS>  
F:30-130/Domain: propeptide #status predicted <PRO>  
F:131-173/Product: neutrophil antibiotic protein Bac5 #status predicted <MAT>  
F:173/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 39.5%; Score 94; DB 2; Length 176;  
Best Local Similarity 54.1%; Pred. No. 0.055;  
Matches 20; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 3 RRPYPYLPRRPPPPFFPPRLPPRIPPGGFPPRFPFRFP 39  
| | | | | | | | | | | | | | | | | | | | | |  
Db 131 RFRPPIRRPPIRPPFYPPFRPPIRPPIFPPIRPPFRP 167

RESULT 14

A36589

bactenecin 7 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-May-1997  
C:Accession: A36589  
R:Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.  
J. Biol. Chem. 265, 18871-18874, 1990  
A:Title: Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of  
A:Reference number: A36589; MUID:91035404; PMID:2229048  
A:Accession: A36589  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-59 <FRA>  
C:Superfamily: cathelin; cystatin homology

Query Match 39.1%; Score 93; DB 2; Length 59;  
Best Local Similarity 61.5%; Pred. No. 0.025;  
Matches 24; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 RRRRPPPYLPRRPPPPFFPPRLPPR-IPPGFP-PRFP 37  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 RIRPRPRLPRRPRRPLPFP RPGRPIRPLPFP RPGR 40

RESULT 15

S39206

proline-rich protein V-beta 1 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: A53118; S39206  
R:Courty, Y.; Rosinski-Chupin, I.; Rougeon, F.  
J. Biol. Chem. 269, 520-527, 1994  
A:Title: A new proline-rich protein precursor expressed in the salivary glands of the rat  
A:Reference number: A53118; MUID:94103265; PMID:8276845  
A:Accession: A53118  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-148 <COU>  
A:Cross-references: UNIPROT:Q64371; EMBL:X74229; NID:g433616; PIDN:CAA52300.1; PID:g43361  
A>Note: submitted to the EMBL Data Library, July 1993

**C;Genetics:**

A: Introns: 18/3

C: Superfamily: proline-rich peptide P-B

E:1-18/Domain: signal sec

F:133.143/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;133,143/BIRMINGHAM sec: carbon/yaraco (now) "COAL-CONC")

Query Match  
Best local similarity 52.3%  
Score 36.9%  
Pred No. 0.063

Matches 23; Conservative 0; Mismatches 12; Indels 9; Gaps 3;

Qy  
1 RRRPPPYLPRPPPPF-----FPPRLPPRIppGFFPPRFFppRFP 39

Db 32 RRRPPP--PPPPPPFFGGIGQPP--PPHFGFGFP PPPP 71

Job time : 31.0727 secs

DATE : 21/07/2023

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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:52:03 ; Search time 135.082 Seconds  
(without alignments)  
147.844 Million cell updates/sec

Title: US-10-014-147-1  
Perfect score: 238  
Sequence: 1 RRRPRPPYLRPPPPPPPPRRLPPRIPPPPPPPRFP 39

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	238	100.0	172	1	PR39_PIG	P80054 sus scrofa
2	127.5	53.6	484	2	Q8ILQ0	Q8ilq0 plasmodium
3	118	49.6	333	2	Q9XI23	Q9xi23 oryza sativ
4	110.5	46.4	415	2	Q7RQA0	Q7rqa0 plasmodium
5	109.5	46.0	212	1	PF11_PIG	P51524 sus scrofa
6	108.5	45.6	236	2	Q657Y0	Q657y0 oryza sativ
7	107.5	45.2	93	2	Q61649	Q61649 onchocerca
8	107	45.0	301	2	Q41848	Q41848 zea mays (m
9	106	44.5	409	2	Q9SBM1	Q9sbm1 volvox cart
10	105.5	44.3	997	2	Q9GYL4	Q9gyl4 caenorhabdi
11	103	43.3	351	2	Q84Q90	Q84q90 oryza sativ
12	102.5	43.1	228	1	PF12_PIG	P51525 sus scrofa
13	102.5	43.1	640	2	Q6P0D5	Q6p0d5 brachydanio
14	102	42.9	890	2	Q80W14	Q80w14 mus musculu
15	101.5	42.6	135	2	Q61134	Q61134 dictyosteli
16	101.5	42.6	139	2	Q61135	Q61135 dictyosteli
17	101.5	42.6	389	2	Q88539	Q88539 mus musculu
18	101.5	42.6	400	2	Q96AY8	Q96ay8 homo sapien
19	101.5	42.6	532	2	Q61133	Q61133 dictyosteli
20	101.5	42.6	628	2	Q6PF41	Q6pf41 xenopus lae
21	101.5	42.6	635	2	Q6NTV3	Q6ntv3 xenopus lae
22	101.5	42.6	636	2	Q6GL09	Q6gl09 xenopus tro
23	101.5	42.6	641	2	Q9Y2W2	Q9y2w2 homo sapien
24	101.5	42.6	641	2	Q923D5	Q923d5 mus musculu
25	101.5	42.6	641	2	Q8VDI0	Q8vdi0 m.wv domain
26	100.5	42.2	150	2	Q67VV4	Q67vv4 oryza sativ
27	99.5	41.8	150	2	Q6Z4P0	Q6z4p0 oryza sativ
28	99	41.6	1395	2	Q7SC01	Q7sc01 neurospora
29	98	41.2	1006	2	Q9LMQ1	Q9lmq1 arabidopsis
30	97.5	41.0	134	2	Q9XIP3	Q9xip3 arabidopsis
31	97.5	41.0	210	2	Q6ZJE9	Q6zje9 oryza sativ

32	97.5	41.0	3889	2	Q6SSE8	Q6sse8 chlamydomon
33	97	40.8	158	2	Q9DVM0	Q9dvw0 plutella xy
34	97	40.8	881	2	Q6H7U3	Q6h7u3 oryza sativ
35	96	40.3	181	2	Q35328	Q35328 mus musculu
36	96	40.3	1386	1	ZAP3_MOUSE	Q9r017 mus musculu
37	95.5	40.1	381	1	PRLP_BOVIN	Q9gkn8 bos taurus
38	95.5	40.1	608	2	Q69S58	Q69s58 oryza sativ
39	95.5	40.1	1134	2	Q96JH1	Q96jh1 homo sapien
40	95	39.9	342	2	Q6ZD62	Q6zd62 oryza sativ
41	95	39.9	439	2	Q42421	Q42421 beta vulgar
42	95	39.9	520	2	Q86YA8	Q86ya8 homo sapien
43	95	39.9	723	2	Q8NBB9	Q8nbb9 homo sapien
44	95	39.9	1766	2	Q8NF45	Q8nf45 homo sapien
45	94.5	39.7	146	2	Q7Q8P5	Q7q8p5 anopheles g

ALIGNMENTS

RESULT 1  
PR39\_PIG STANDARD; PRT; 172 AA.  
AC P80054; Q9TR84;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antibacterial protein PR-39 precursor.  
GN Name=PR39;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=95350216; PubMed=7624374;  
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,  
Andersson L., Boman H.G.;  
RT "Structure of the gene for porcine peptide antibiotic PR-39, a  
cathelin gene family member: comparative mapping of the locus for the  
human peptide antibiotic FALL-39.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).  
RN [2]  
SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=94071853; PubMed=8250863;  
RA Storici P., Zanetti M.;  
RT "A CDNA derived from pig bone marrow cells predicts a sequence  
identical to the intestinal antibacterial peptide PR-39.";  
RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).  
RN [3]  
SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;  
RA Zhao C., Ganz T., Lehrer R.I.;  
RT "Structures of genes for two cathelin-associated antimicrobial  
peptides: prophenin-2 and PR-39.";  
RL FEBS Lett. 376:130-134(1995).  
RN [4]  
SEQUENCE OF 131-169.  
RC TISSUE=Intestine;  
RX MEDLINE=92111534; PubMed=1765098;  
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,  
Mutt V., Joernvall H.;  
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new  
member of the family of proline-arginine-rich antibacterial  
peptides.";  
RL Eur. J. Biochem. 202:849-854(1991).  
RN [5]  
SEQUENCE OF 131-164, AND FUNCTION.  
RC TISSUE=Neutrophils;  
RX MEDLINE=95088504; PubMed=7996056;  
RA Shi J., Ross C.R., Chengappa M.M., Blecha F.;  
RT "Identification of a proline-arginine-rich antibacterial peptide from









RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Miller N.;  
RT "The sequence of C. elegans cosmid R04E5.";  
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Wilson R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RG WormBase Consortium;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U41538; AAG00010.1; -.  
DR PIR; T28872; T28872.  
DR WormBase; WBGene00019871; R04E5.8.  
DR WormPep; R04E5.8a; CE04800.  
KW Hypothetical protein.  
SQ SEQUENCE 997 AA; 111954 MW; F1620378EF0D9DB6 CRC64;

Query Match 44.3%; Score 105.5; DB 2; Length 997;  
Best Local Similarity 55.8%; Pred. No. 0.29;  
Matches 24; Conservative 0; Mismatches 14; Indels 5; Gaps 2;

QY 2 RRPR--PPYLPRPPPPPPPP---RLPPRIPPGFFPPRFP 39  
DB 145 RVPRTPPPRRPPPPPPPPPPPPPPPPPPPPPPPPPP 187

RESULT 11  
Q84Q90 PRELIMINARY; PRT; 351 AA.  
AC Q84Q90;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein OJ1041F02.15.  
GN Name=OJ1041F02.15;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,  
Collura K.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC135206; AAP06858.1; -.  
DR Gramene; Q84Q90; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR InterPro; IPR007087; Znf\_C2H2.  
DR InterPro; IPR000690; Znf\_matrin.  
DR InterPro; IPR003604; Znf\_U1.  
DR SMART; SM00355; ZnP\_C2H2; 1.  
DR SMART; SM00451; Znf\_U1; 1.  
DR PROSITE; PS50171; ZF\_MATRIN; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 351 AA; 38984 MW; 4DE76B97D657701B CRC64;

Query Match 43.3%; Score 103; DB 2; Length 351;  
Best Local Similarity 57.6%; Pred. No. 0.18;

Matches 19; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 4 PRPPYLPRPPPPPPPPPPRLPPRIPPGFFPPRFP 36  
DB 265 PRPPPPQVPPPPPPQAPPPPPPNAPMGMPRIPP 297  
RESULT 12  
PF12\_PIG STANDARD; PRT; 228 AA.  
AC P51525;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Prophenin-2 precursor (PF-2) (PR-2) (C12) (Prophenin-1 like).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=94085623; PubMed=8262247; DOI=10.1016/0014-5793(93)80821-B;  
RA Pungercar J., Strukelj B., Kopitar G., Renko M., Lenarcic B.,  
Gubensek F., Turk V.;  
RT "Molecular cloning of a putative homolog of proline/arginine-rich  
antibacterial peptides from porcine bone marrow.";  
RL FEBS Lett. 336:284-288(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;  
RA Zhao C., Ganz T., Lehrer R.I.;  
RT "Structures of genes for two cathelin-associated antimicrobial  
peptides: prophenin-2 and PR-39.";  
RL FEBS Lett. 376:130-134(1995).  
CC -!- FUNCTION: Exerts antimicrobial activity. It is more effective  
CC against Gram-negative bacteria than Gram-positive bacteria.  
CC -!- SIMILARITY: Belongs to the cathelicidin family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X75438; CAA53188.1; -.  
DR EMBL; X89202; CAA61488.1; -.  
DR PIR; S40463; S40463.  
DR HSSP; P32196; 1KWI.  
DR InterPro; IPR001894; Cathelicidin.  
DR Pfam; PF00666; Cathelicidins; 1.  
DR ProDom; PD001838; Cathelicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
KW Amidation; Antibiotic; Pyrrolidone carboxylic acid; Repeat; Signal.  
FT SIGNAL 1 29 Potential.  
FT PROPEP 30 146 Potential.  
FT PEPTIDE 147 225 Prophenin-2.  
FT PROPEP 226 228 Removed in mature form (Potential).  
FT MOD\_RES 225 225 Proline amide (G-226 provides amide  
FT group) (Potential).  
FT DOMAIN 132 228 Pro-rich.  
FT DOMAIN 148 217 7 X 10 AA tandem repeats.  
FT REPEAT 148 157 1.  
FT REPEAT 158 167 2.  
FT REPEAT 168 177 3.  
FT REPEAT 178 187 4.  
FT REPEAT 188 197 5.  
FT REPEAT 198 207 6.  
FT REPEAT 208 217 7.





OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WS576;  
RX MEDLINE=98367519; PubMed=9692967; DOI=10.1021/bi9808013;  
RA Zhang Y., Brown R.D. Jr., West C.M.;  
RT "Two proteins of the Dictyostelium spore coat bind to cellulose in vitro."  
RL Biochemistry 37:10766-10779(1998).  
DR EMBL; AF066072; AAC19124.1; -.  
DR DictyBase; DDB0185060; pspsB.  
FT NON\_TER 1  
FT NON\_TER 135  
SQ SEQUENCE 135 AA; 14829 MW; 500634A988A49408 CRC64;  
  
Query Match 42.6%; Score 101.5; DB 2; Length 135;  
Best Local Similarity 44.7%; Pred. No. 0.095;  
Matches 17; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 5 RPPYLPRPRP---PPFPRLPPRIPPGFPFRFPFRFP 39  
Db 21 QPPTYPTQPPTQPTYPSPSYPPSYPTYPPTHPPTYP 58

Search completed: October 26, 2005, 05:18:30  
Job time : 140.082 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 40.0636 Seconds  
(without alignments)  
72.667 Million cell updates/sec

Title: US-10-014-147-1  
Perfect score: 238  
Sequence: 1 RRRPRPPYLPRPPPPFFPPRLPPRIPGPPPPRFRFP 39

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	100.0	39	1 US-08-162-052-1	Sequence 1, Appli
2	238	100.0	39	1 US-08-310-722-1	Sequence 1, Appli
3	238	100.0	39	2 US-08-419-066-1	Sequence 1, Appli
4	238	100.0	39	2 US-08-728-333-1	Sequence 1, Appli
5	238	100.0	39	3 US-09-024-975-1	Sequence 1, Appli
6	238	100.0	39	4 US-08-930-777A-1	Sequence 1, Appli
7	238	100.0	39	5 PCT-US95-12080-1	Sequence 1, Appli
8	221.5	93.1	38	4 US-09-739-535-1	Sequence 1, Appli
9	155	65.1	26	2 US-08-419-066-2	Sequence 2, Appli
10	155	65.1	26	3 US-09-024-975-2	Sequence 2, Appli
11	155	65.1	26	4 US-08-930-777A-2	Sequence 2, Appli
12	140	58.8	23	4 US-08-930-777A-3	Sequence 3, Appli
13	116	48.7	19	4 US-08-930-777A-4	Sequence 4, Appli
14	106	44.5	78	1 US-08-487-359-5	Sequence 5, Appli
15	106	44.5	78	1 US-08-222-798A-5	Sequence 5, Appli
16	101.5	42.6	311	3 US-09-179-558-66	Sequence 66, Appl
17	101.5	42.6	311	4 US-09-722-825-66	Sequence 66, Appl
18	101.5	42.6	311	4 US-09-722-487-66	Sequence 66, Appl
19	101.5	42.6	311	4 US-09-722-708-66	Sequence 66, Appl
20	101	42.4	79	1 US-08-487-359-1	Sequence 1, Appli
21	101	42.4	79	1 US-08-487-359-3	Sequence 3, Appli
22	101	42.4	79	1 US-08-487-359-8	Sequence 8, Appli
23	101	42.4	79	1 US-08-222-798A-1	Sequence 1, Appli
24	101	42.4	79	1 US-08-222-798A-3	Sequence 3, Appli
25	101	42.4	79	1 US-08-222-798A-8	Sequence 8, Appli
26	98.5	41.4	42	4 US-09-030-619-162	Sequence 162, App
27	98.5	41.4	79	1 US-08-487-359-2	Sequence 2, Appli

28	98.5	41.4	79	1	US-08-487-359-4	Sequence 4, Appli
29	98.5	41.4	79	1	US-08-222-798A-2	Sequence 2, Appli
30	98.5	41.4	79	1	US-08-222-798A-4	Sequence 4, Appli
31	96	40.3	16	3	US-09-024-975-3	Sequence 3, Appli
32	96	40.3	16	4	US-08-930-777A-5	Sequence 5, Appli
33	96	40.3	76	4	US-09-547-693-233	Sequence 233, App
34	95	39.9	78	1	US-08-487-359-7	Sequence 7, Appli
35	95	39.9	78	1	US-08-222-798A-7	Sequence 7, Appli
36	94.5	39.7	424	4	US-09-949-016-7950	Sequence 7950, Ap
37	94	39.5	43	3	US-09-024-975-7	Sequence 7, Appli
38	94	39.5	43	5	PCT-US95-12080-2	Sequence 2, Appli
39	94	39.5	79	1	US-08-487-359-6	Sequence 6, Appli
40	94	39.5	79	1	US-08-222-798A-6	Sequence 6, Appli
41	94	39.5	176	4	US-09-917-340-28	Sequence 28, Appl
42	94	39.5	288	4	US-09-270-767-42632	Sequence 42632, A
43	93	39.1	59	4	US-09-030-619-163	Sequence 163, App
44	92.5	38.9	498	4	US-09-949-016-7108	Sequence 7108, Ap
45	92	38.7	15	4	US-08-930-777A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-08-162-052-1  
; Sequence 1, Application US/08162052  
; Patent No. 5489575  
; GENERAL INFORMATION:  
; APPLICANT: LEE, Jong-Youn  
; APPLICANT: BOMAN, Hans G  
; APPLICANT: MUTT, Viktor  
; APPLICANT: JORNVAL, Hans  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/162,052  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9101838-2  
; FILING DATE: 14-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO 92-22578  
; FILING DATE: 23-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crane-Feury, Sharon E  
; REGISTRATION NUMBER: 36,113  
; REFERENCE/DOCKET NUMBER: 003300-299  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-162-052-1

Query Match 100.0%; Score 238; DB 1; Length 39;

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Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPPPPPPPPRLPPRIPPGFPPPPRFRFP 39
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Db 1 RRRPRPPYLPRPPPPPPPPRLPPRIPPGFPPPPRFRFP 39

RESULT 2
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jornvall, Hans
; TITLE: No. 5654273el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-310-722-1

Query Match 100.0%; Score 238; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RRRPRPPYLPRPPPPPPPPRLPPRIPPGFPPPPRFRFP 39

RESULT 3
US-08-419-066-1
; Sequence 1, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
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; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-1

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Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RRRPRPPYLPRPPPPPPPPRLPPRIPPGFPPPPRFRFP 39

RESULT 4
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; Sequence 1, Application US/08728333
; Patent No. 5863897
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,333
; FILING DATE:
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CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/310,722  
FILING DATE: 22-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: CMCC379  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-815-6508  
TELEFAX: (404)-815-6555  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PUBLICATION INFORMATION:  
AUTHORS: Lee, Jong-Youn  
AUTHORS: Boman, Hans G.  
AUTHORS: Mutt, Viktor  
AUTHORS: Jornvall, Hans  
TITLE: No. 5863897el Polypeptides And Their Use  
JOURNAL: PCT WO 92/23578  
DATE: 12/23/92  
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39  
US-08-728-333-1

Query Match 100.0%; Score 238; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.6e-17;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RRRPRPPYLPRPPPPPPRRLPPRIIPPGFPPRPPRFP 39

RESULT 5  
US-09-024-975-1  
Sequence 1, Application US/09024975  
Patent No. 6133233  
GENERAL INFORMATION:  
APPLICANT: ROSS, CHRISTOPHER R.  
APPLICANT: BLECHA, FRANK  
APPLICANT: SHI, JISHU  
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
STREET: 2405 GRAND BLVD., SUITE 400  
CITY: KANSAS CITY  
STATE: MO  
COUNTRY: USA  
ZIP: 64108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,975  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/802,306  
FILING DATE: 18-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COLLINS, JOHN M.  
REGISTRATION NUMBER: 26,262  
REFERENCE/DOCKET NUMBER: 25585-A  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 816/474-9050  
TELEFAX: 816/474-9057  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-024-975-1

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Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6  
US-08-930-777A-1  
Sequence 1, Application US/08930777A  
Patent No. 6713605  
GENERAL INFORMATION:  
APPLICANT: Blecha, Frank  
APPLICANT: Shi, Jishu  
TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hovey, Williams, Timmons & Collins  
STREET: 2405 Grand Blvd., Ste. 400  
CITY: Kansas City  
STATE: Missouri  
COUNTRY: U.S.A.  
ZIP: 64108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,777A  
FILING DATE: October 8, 1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/04674  
FILING DATE: April 10, 1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26,262  
REFERENCE/DOCKET NUMBER: 23625-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-930-777A-1

Query Match 100.0%; Score 238; DB 4; Length 39;  
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Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7



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Best Local Similarity 100.0%; Pred. No. 9.4e-08;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



SEQUENCE CHARACTERISTICS:  
LENGTH: 78 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-222-798A-5

Query Match 44.5%; Score 106; DB 1; Length 78;  
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Db 10 PRFPFPQFGPRFPNFPNFGPRFP---PPQFGFRFPFPFP 47

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113.119 Million cell updates/sec

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Perfect score: 238  
Sequence: 1 RRRPRPPVLP RRRPPPPFPFPPRLPRIPPPFPFPPRFP 39

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Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	238	100.0	39	15	US-10-391-155-1
3	238	100.0	39	15	US-10-391-155-2
4	238	100.0	39	15	US-10-391-155-6
5	238	100.0	39	15	US-10-651-147-1
6	238	100.0	42	16	US-10-344-709C-18
7	238	100.0	42	17	US-10-916-185-14
8	238	100.0	42	18	US-10-991-286A-44
9	238	100.0	42	20	US-11-004-379-20
10	221.5	93.1	38	9	US-09-738-742-1
11	221.5	93.1	38	9	US-09-739-535-1
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					Sequence 1, Appli
					Sequence 2, Appli
					Sequence 6, Appli
					Sequence 1, Appli
					Sequence 18, Appl
					Sequence 14, Appl
					Sequence 44, Appl
					Sequence 20, Appl
					Sequence 1, Appli
					Sequence 1, Appli

12	155	65.1	26	14	US-10-014-147-2	Sequence 2, Appli
13	155	65.1	26	15	US-10-651-147-2	Sequence 2, Appli
14	140	58.8	23	14	US-10-014-147-3	Sequence 3, Appli
15	140	58.8	23	15	US-10-651-147-3	Sequence 3, Appli
16	119.5	50.2	483	16	US-10-437-963-191498	Sequence 191498,
17	119	50.0	91	16	US-10-425-115-200180	Sequence 200180,
18	118	49.6	83	16	US-10-437-963-118176	Sequence 118176,
19	118	49.6	333	16	US-10-437-963-191891	Sequence 191891,
20	116	48.7	19	14	US-10-014-147-4	Sequence 4, Appli
21	116	48.7	19	15	US-10-651-147-4	Sequence 4, Appli
22	116	48.7	276	16	US-10-437-963-132896	Sequence 132896,
23	114	47.9	200	16	US-10-425-115-206766	Sequence 206766,
24	114	47.9	245	16	US-10-425-115-206869	Sequence 206869,
25	111	46.6	159	16	US-10-425-115-320315	Sequence 320315,
26	111	46.6	323	16	US-10-437-963-175653	Sequence 175653,
27	111	46.6	431	16	US-10-437-963-204963	Sequence 204963,
28	110.5	46.4	96	16	US-10-437-963-120965	Sequence 120965,
29	110.5	46.4	204	16	US-10-437-963-180133	Sequence 180133,
30	109	45.8	173	16	US-10-437-963-191890	Sequence 191890,
31	108	45.4	91	16	US-10-437-963-160130	Sequence 160130,
32	108	45.4	136	16	US-10-425-115-222187	Sequence 222187,
33	107	45.0	270	16	US-10-437-963-197222	Sequence 197222,
34	107	45.0	322	16	US-10-425-115-316075	Sequence 316075,
35	106	44.5	151	16	US-10-437-963-134683	Sequence 134683,
36	106	44.5	153	15	US-10-425-114-53570	Sequence 53570, A
37	106	44.5	321	16	US-10-425-115-202316	Sequence 202316,
38	106	44.5	329	16	US-10-437-963-163296	Sequence 163296,
39	106	44.5	621	16	US-10-437-963-177697	Sequence 177697,
40	105.5	44.3	215	16	US-10-767-701-35371	Sequence 35371, A
41	105.5	44.3	224	16	US-10-425-115-289952	Sequence 289952,
42	105	44.1	87	14	US-10-029-386-30727	Sequence 30727, A
43	105	44.1	156	15	US-10-424-599-144804	Sequence 144804,
44	105	44.1	180	15	US-10-424-599-242969	Sequence 242969,
45	104.5	43.9	76	16	US-10-425-115-236218	Sequence 236218,

ALIGNMENTS

RESULT 1  
US-10-014-147-1  
; Sequence 1, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/014,147  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A





APPLICATION NUMBER: US/10/391,155  
FILING DATE: 18-Mar-2003  
CLASSIFICATION: Unknown  
ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker, Esq.  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: BIS-044/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 100.0%; Score 238; DB 15; Length 39;  
Best Local Similarity 100.0%; Pred. No. 8.1e-14;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPPPPPPRLPPRIPPGFPPRPFRFP 39  
Db 1 RRRPRPPYLPRPPPPPPRLPPRIPPGFPPRPFRFP 39

RESULT 5  
US-10-651-147-1  
; Sequence 1, Application US/10651147  
; Publication No. US20040043934A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
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; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/651,147  
; FILING DATE: 28-Aug-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
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; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
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US-10-651-147-1

Query Match 100.0%; Score 238; DB 15; Length 39;  
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RESULT 6  
US-10-344-709C-18  
; Sequence 18, Application US/10344709C  
; Publication No. US20040170642A1  
; GENERAL INFORMATION:  
; APPLICANT: JORG FRITZ ET AL.  
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin  
; TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof  
; FILE REFERENCE: SONN:030US  
; CURRENT APPLICATION NUMBER: US/10/344,709C  
; PRIOR FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP01/09529  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: A 1416/2000  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
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; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-344-709C-18

Query Match 100.0%; Score 238; DB 16; Length 42;  
Best Local Similarity 100.0%; Pred. No. 8.6e-14;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPPPPPPRLPPRIPPGFPPRPFRFP 39  
Db 1 RRRPRPPYLPRPPPPPPRLPPRIPPGFPPRPFRFP 39

RESULT 7  
US-10-916-185-14  
; Sequence 14, Application US/10916185  
; Publication No. US20050107325A1  
; GENERAL INFORMATION:  
; APPLICANT: Manoharan, Muthiah  
; APPLICANT: Kesavan, Venkitasamy  
; APPLICANT: Rajeev, Kallanthottathil G.  
; TITLE OF INVENTION: MODIFIED iRNA AGENTS  
; FILE REFERENCE: 14174-091001  
; CURRENT APPLICATION NUMBER: US/10/916,185  
; CURRENT FILING DATE: 2004-08-10  
; PRIOR APPLICATION NUMBER: PCT/US2004/011829  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 60/465,665  
; PRIOR FILING DATE: 2003-04-25  
; PRIOR APPLICATION NUMBER: US 60/463,772  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: US 60/469,612  
; PRIOR FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/465,802  
; PRIOR FILING DATE: 2003-04-25  
; PRIOR APPLICATION NUMBER: US 60/493,986  
; PRIOR FILING DATE: 2003-08-08  
; PRIOR APPLICATION NUMBER: US 60/494,597  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: US 60/503,414  
; PRIOR FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 60/506,341

; PRIOR FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: US 60/510,246  
; PRIOR FILING DATE: 2003-10-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Exemplary Cell Permeation Peptides  
US-10-916-185-14

Query Match 100.0%; Score 238; DB 17; Length 42;  
Best Local Similarity 100.0%; Pred. No. 8.6e-14;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRPPYLP... 39  
Db 1 RRRRPPYLP... 39

RESULT 8  
US-10-991-286A-44  
; Sequence 44, Application US/10991286A  
; Publication No. US20050186591A1  
; GENERAL INFORMATION:  
; APPLICANT: Bumcrot, David  
; APPLICANT: Farrer, Matthew J.  
; APPLICANT: Maraganore, Demetrius M.  
; APPLICANT: Vornlocher, Hans-Peter  
; TITLE OF INVENTION: METHOD OF TREATING NEURODEGENERATIVE DISEASE  
; FILE REFERENCE: 17574-003001  
; CURRENT APPLICATION NUMBER: US/10/991,286A  
; CURRENT FILING DATE: 2004-11-17  
; PRIOR APPLICATION NUMBER: PCT/US2004/18271  
; PRIOR FILING DATE: 2004-06-09  
; PRIOR APPLICATION NUMBER: US 60/476,947  
; PRIOR FILING DATE: 2003-06-09  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Exemplary Cell Permeation Peptide  
US-10-991-286A-44

Query Match 100.0%; Score 238; DB 18; Length 42;  
Best Local Similarity 100.0%; Pred. No. 8.6e-14;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRPPYLP... 39  
Db 1 RRRRPPYLP... 39

RESULT 9  
US-11-004-379-20  
; Sequence 20, Application US/11004379  
; Publication No. US2005015337A1  
; GENERAL INFORMATION:  
; APPLICANT: Manoharan, Muthiah  
; TITLE OF INVENTION: iRNA CONJUGATES  
; FILE REFERENCE: 14174-067001  
; CURRENT APPLICATION NUMBER: US/11/004,379  
; CURRENT FILING DATE: 2004-12-03  
; PRIOR APPLICATION NUMBER: PCT/US04/10586  
; PRIOR FILING DATE: 2004-04-05  
; PRIOR APPLICATION NUMBER: US 60/460,783  
; PRIOR FILING DATE: 2003-04-03

; PRIOR APPLICATION NUMBER: US 60/462,894  
; PRIOR FILING DATE: 2003-04-14  
; PRIOR APPLICATION NUMBER: US 60/465,665  
; PRIOR FILING DATE: 2003-04-25  
; PRIOR APPLICATION NUMBER: US 60/463,772  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: US 60/469,612  
; PRIOR FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/503,414  
; PRIOR FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 60/465,802  
; PRIOR FILING DATE: 2003-04-25  
; PRIOR APPLICATION NUMBER: US 60/493,986  
; PRIOR FILING DATE: 2003-08-08  
; PRIOR APPLICATION NUMBER: US 60/494,597  
; PRIOR FILING DATE: 2003-08-11  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Exemplary Cell Permeation Peptides  
US-11-004-379-20

Query Match 100.0%; Score 238; DB 20; Length 42;  
Best Local Similarity 100.0%; Pred. No. 8.6e-14;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRPPYLP... 39  
Db 1 RRRRPPYLP... 39

RESULT 10  
US-09-738-742-1  
; Sequence 1, Application US/09738742  
; Publication No. US20020025924A1  
; GENERAL INFORMATION:  
; APPLICANT: Cubist Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS  
; FILE REFERENCE: C060  
; CURRENT APPLICATION NUMBER: US/09/738,742  
; CURRENT FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-738-742-1

Query Match 93.1%; Score 221.5; DB 9; Length 38;  
Best Local Similarity 97.4%; Pred. No. 2.1e-12;  
Matches 38; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 RRRRPPYLP... 39  
Db 1 RRRRPPYLP... 38

RESULT 11  
US-09-739-535-1  
; Sequence 1, Application US/09739535  
; Publication No. US2002005878A1  
; GENERAL INFORMATION:  
; APPLICANT: Cubist Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS  
; FILE REFERENCE: C060

;; CURRENT APPLICATION NUMBER: US/09/739,535  
;; CURRENT FILING DATE: 2000-12-15  
;; NUMBER OF SEQ ID NOS: 1  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1  
;; LENGTH: 38  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic  
US-09-739-535-1  
  
Query Match 93.1%; Score 221.5; DB 9; Length 38;  
Best Local Similarity 97.4%; Pred. No. 2.1e-12;  
Matches 38; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 RRRPRPPYLPRPPPPPPRLPPRIPPFGPPRPPRFP 39  
Db 1 RRRPRPPYLPRPPPPPPPPRLPPRIPP-FPPRFP 38  
  
RESULT 12  
US-10-014-147-2  
; Sequence 2, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/014,147  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-014-147-2  
  
Query Match 65.1%; Score 155; DB 14; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.4e-07;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRRPRPPYLPRPPPPPPPPRLPPRI 26  
Db 1 RRRPRPPYLPRPPPPPPPPRLPPRI 26  
  
RESULT 14  
US-10-014-147-3  
; Sequence 3, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.

Db 1 RRRPRPPYLPRPPPPPPPPRLPPRI 26  
  
RESULT 13  
US-10-651-147-2  
; Sequence 2, Application US/10651147  
; Publication No. US20040043934A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/651,147  
; FILING DATE: 28-Aug-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-651-147-2  
  
Query Match 65.1%; Score 155; DB 15; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.4e-07;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRRPRPPYLPRPPPPPPPPRLPPRI 26  
Db 1 RRRPRPPYLPRPPPPPPPPRLPPRI 26  
  
RESULT 14  
US-10-014-147-3  
; Sequence 3, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.

ZIP: 64108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/014,147  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,777A  
FILING DATE: October 8, 1997  
APPLICATION NUMBER: PCT/US96/04674  
FILING DATE: April 10, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26,262  
REFERENCE/DOCKET NUMBER: 23625-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-014-147-3

Query Match 58.8%; Score 140; DB 14; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PRPPYLPRPRPPPPPPRLPPRI 26  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 PRPPYLPRPRPPPPPPPPRLPPRI 23

RESULT 15  
US-10-651-147-3  
; Sequence 3, Application US/10651147  
; Publication No. US20040043934A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/651,147  
; FILING DATE: 28-Aug-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-651-147-3  
Query Match 58.8%; Score 140; DB 15; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PRPPYLPRPRPPPPPPRLPPRI 26  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 PRPPYLPRPRPPPPPPPPRLPPRI 23  
Search completed: October 26, 2005, 05:28:55  
Job time : 152.945 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:51:43 ; Search time 102.345 Seconds  
(without alignments)  
98.253 Million cell updates/sec

Title: US-10-014-147-2  
Perfect score: 155  
Sequence: 1 RRRPRPPYLRRPRPPFFPPRLPPRI 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	100.0	26	AAW01447	Aaw01447 Leukocyte
2	155	100.0	26	AAW75723	Aaw75723 Proline-a
3	155	100.0	26	ADe86113	Ade86113 Proline-a
4	155	100.0	26	ADL67255	Adl67255 Antimicro
5	155	100.0	39	AAR30491	Aar30491 Antibacte
6	155	100.0	39	AAR99121	Aar99121 Magainin-
7	155	100.0	39	AAR94446	Aar94446 Synducin
8	155	100.0	39	AAW01446	Aaw01446 Leukocyte
9	155	100.0	39	AAW75722	Aaw75722 Proline/A
10	155	100.0	39	AAAB26888	Aab26888 PR-39 pep
11	155	100.0	39	AAAB97280	Aab97280 PR-39 pep
12	155	100.0	39	AAAB84690	Aab84690 Amino aci
13	155	100.0	39	ADD35364	Add35364 Antimicro
14	155	100.0	39	ADE86112	Ade86112 Proline-a
15	155	100.0	39	ADL67254	Adl67254 Antimicro
16	155	100.0	42	ABBO7714	Abb07714 Antimicro
17	155	100.0	42	ADR82250	Adr82250 Cell perm
18	155	100.0	44	AAAB51194	Aab51194 E. coli A
19	140	90.3	23	AAW01451	Aaw01451 Leukocyte
20	140	90.3	23	ADE86114	Ade86114 Proline-a
21	140	90.3	23	ADL67256	Adl67256 Antimicro
22	116	74.8	19	AAW01452	Aaw01452 Leukocyte
23	116	74.8	19	ADE86115	Ade86115 Proline-a
24	116	74.8	19	ADL67257	Adl67257 Antimicro
25	96	61.9	16	AAW01448	Aaw01448 Leukocyte

26	96	61.9	16	2	AAW75724	Aaw75724 Proline/A
27	96	61.9	16	8	ADe86116	Ade86116 Proline-a
28	96	61.9	16	8	ADL67258	Adl67258 Antimicro
29	90	58.1	15	3	AAAB26885	Aab26885 PR-39 der
30	90	58.1	15	4	AAAB97277	Aab97277 PR-39 der
31	90	58.1	15	4	AAAB84691	Aab84691 Amino aci
32	83	53.5	14	2	AAW01450	Aaw01450 Leukocyte
33	83	53.5	14	2	AAW75725	Aaw75725 Proline/A
34	83	53.5	14	8	ADE86118	Ade86118 Proline-a
35	83	53.5	14	8	ADL67260	Adl67260 Antimicro
36	82	52.9	35	2	AAR79212	Aar79212 Bacteneci
37	82	52.9	59	2	AAW66400	Aaw66400 Cationic
38	82	52.9	59	3	AAAY91699	Aay91699 Cationic
39	82	52.9	59	6	ABU59576	Abu59576 Cationic
40	82	52.9	60	5	ABB07713	Abb07713 Antimicro
41	82	52.9	62	4	AAAB51197	Aab51197 E. coli A
42	78	50.3	278	2	AAAR79095	Aar79095 Rat Fas 1
43	78	50.3	278	2	AAAW98069	Aaw98069 Rat Fas 1
44	78	50.3	278	2	AAAW95040	Aaw95040 Rat FasL
45	78	50.3	278	5	AAAO19029	Aao19029 Human Fas

ALIGNMENTS

RESULT 1  
AAW01447  
ID AAW01447 standard; peptide; 26 AA.  
XX  
AC AAW01447;  
XX  
DT 18-JUN-1997 (first entry)  
XX  
DE Leukocyte O2- production inhibitor peptide PR26.  
XX  
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;  
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;  
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;  
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;  
KW tissue damage; oxygen radical; inflammatory disease; therapy.  
XX  
OS Synthetic.  
XX  
PN WO9632129-A1.  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-US004674.  
XX  
PR 10-APR-1995; 95US-00419066.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 1996-476842/47.  
XX  
PT Inhibition of leukocyte super:oxide anion prodn. and attraction of  
leukocytes - using peptide(s) partic. based on antimicrobial PR-39.  
XX  
PS Claim 3; Page 26; 45pp; English.  
XX  
CC AAW01447-W01454 represent fragments of the proline-arginine rich  
antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first  
isolated from porcine small intestine, and has also been identified in  
human and porcine neutrophils. PR39 kills bacteria by interfering with  
DNA and/or protein synthesis. PR39 also induces syndecan expression on  
mesenchymal cells. Syndecans are important in wound repair, showing that  
PR39 can be used in wound repair, as well as in antibacterial agents.  
CC These sequences, and PR39, can be used in the method of the invention.  
CC The method of the invention is for inhibiting leukocyte superoxide anion  
(O2-) production. The method comprises administering to a leukocyte a  
peptide (such as this sequence) capable of inhibiting leukocyte O2-

CC production. The peptides can be used as medicaments for fighting  
CC infection by attracting leukocytes to a wound site and restricting tissue  
CC damage at the wound site caused by excessive oxygen radicals produced by  
CC these leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states

XX  
SQ Sequence 26 AA;

Query Match	100.0%;	Score 155;	DB 2;	Length 26;
Best Local Similarity	100.0%;	Pred. No. 5.1e-09;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 2  
AAW75723  
ID AAW75723 standard; peptide; 26 AA.

CC The peptides are also useful in connection with surgical procedures such  
CC as coronary bypass and organ transplantation surgery  
XX  
SQ Sequence 26 AA;

RESULT 3  
ADE86113  
ID ADE86113 standard; peptide; 26 AA.



RESULT 4  
ADL67255  
ADL67255 standard; peptide; 26 AA.  
XX  
AC ADL67255;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39 analog PR-26.  
XX  
KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;  
KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;  
KW infection; wound; tissue damage; PR-39 analog; PR-26.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Region 1. .3  
FT /note= "Essential for antibacterial activity"  
FT Region 20. .26  
FT /note= "Essential for antibacterial activity"  
XX  
PN US2004043934-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 28-AUG-2003; 2003US-00651147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 2004-225728/21.  
XX  
PT Inhibiting leukocyte oxygen radical production comprises contacting a  
PT leukocyte with a peptide, where the inhibition occurs as a consequence of  
PT binding between the peptide and p47phox.  
XX  
PS Claim 1; SEQ ID NO 2; 24pp; English.  
XX  
CC The invention relates to inhibiting leukocyte superoxide anion (O2-)  
CC production using a naturally occurring proline-arginine (PR)-rich  
CC antimicrobial peptide known as PR-39 and its truncated analogs. The  
CC method comprises contacting leukocytes with the peptide comprising 39 or  
CC 26 amino acids, for a time and under conditions effective to inhibit  
CC leukocyte superoxide anion production. The peptide inhibits the activity  
CC of NADPH oxidase responsible for anion production, by binding to Src  
CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein  
CC of the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or  
CC porcine leucocyte and the mammalian leucocyte is neutrophil. Another  
CC method is also disclosed which employs a PR-39 analog that comprise 16  
CC amino acids, where the sum of the proline and arginine residues in the  
CC effective peptide is at least 66 or 74 % of the total number of amino  
CC acids. This peptide inhibits leucocyte O2- production by the effective  
CC binding to p47phox in whole cells, therefore interfering with the binding  
CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in  
CC the peptide are arginine residues. The method of the invention is useful  
CC for inhibiting leucocyte oxygen radical production. The peptides are  
CC useful as medicaments for fighting infections by attracting leucocytes to  
CC a wound site, yet restrict tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leucocytes. The present  
XX sequence is PR-39 analog PR-26.  
XX  
SQ Sequence 26 AA;

Query Match 100.0%; Score 155; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 5.1e-09;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRRPPPPFFPPRLPPRI 26  
| | | | | | | | | | | | | | | | | |  
Db 1 RRRPRPPYLP RRRPPPPFFPPRLPPRI 26  
| | | | | | | | | | | | | | | | | |  
RESULT 5  
AAR30491  
ID AAR30491 standard; peptide; 39 AA.  
XX  
AC AAR30491;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-MAY-1993 (first entry)  
XX  
DE Antibacterial peptide.  
XX  
KW Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;  
KW veterinary medicine; prophylactic.  
XX  
OS Sus scrofa domestica.  
XX  
PN WO9222578-A1.  
XX  
PD 23-DEC-1992.  
XX  
PF 10-JUN-1992; 92WO-SE000394.  
XX  
PR 14-JUN-1991; 91SE-00001838.  
XX  
PA (LEEJ/) LEE J.  
PA (BOMA/) BOMAN H G.  
PA (MUTT/) MUTT V.  
PA (JOER/) JOERNVALL H.  
XX  
PI Lee J, Boman HG, Mutt V, Joernvall H;  
XX  
DR WPI; 1993-018080/02.  
XX  
PT New anti-bacterial polypeptide - active against Gram negative bacteria.  
XX  
PS Claim 1; Page 10; 15pp; English.  
XX  
CC This peptide was isolated from the small intestine of a pig. The small  
CC intestine is an important endocrine organ and many physiologically active  
CC peptides have been isolated from it. This peptide inhibits the growth of,  
CC and may kill, bacteria, pref. gram negative bacteria. This peptide or its  
CC functional derivatives may be used in human or veterinary medicine for  
CC therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 39 AA;  
Query Match 100.0%; Score 155; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRRPPPPFFPPRLPPRI 26  
| | | | | | | | | | | | | | | | | |  
Db 1 RRRPRPPYLP RRRPPPPFFPPRLPPRI 26  
| | | | | | | | | | | | | | | | | |  
RESULT 6  
AAR99121  
ID AAR99121 standard; peptide; 39 AA.  
XX  
AC AAR99121;  
XX  
DT 28-OCT-1996 (first entry)  
XX  
DE Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.  
XX



```

proline residue and X is any amino acid residue, which has been found to
inhibit superoxide production, and secondly they have arginine residues
adjacent to these motifs, required for effective inhibition. It was
established by structural and function analysis that a peptide should
ideally contain 4 or 6 of these motifs, and that inhibitory activity is
correlated with the increase of length of peptides. The effectiveness of
these peptides was determined by investigating the production of the
neutrophil superoxide anion, and also the inhibition of neutrophil
chemotaxis. From this, it was found that all of the peptides inhibited
NADPH oxidase to some extent. All of the peptides also inhibit neutrophil
oxidase activity. PR-39 is believed, to be the most potent endogenous
down regulator of NADPH oxidase yet discovered, and from the data
produced, it can be suggested to be involved in eliminating or reducing
the reperfusion injury induced adhesion and extraction of neutrophils.
The peptides are also useful in connection with surgical procedures such
as coronary bypass and organ transplantation surgery
XX
SQ      Sequence 39 AA;
Query Match      100.0%;      Score 155;      DB 2;      Length 39;
Best Local Similarity 100.0%;      Pred. No. 7.2e-09;
Matches 26;      Conservative 0;      Mismatches 0;      Indels 0;      Gaps 0;

Qy      1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26
        |||||
Db      1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26

RESULT 10
AAB26888
ID      AAB26888 standard; peptide; 39 AA.
XX
AC      AAB26888;
XX
DT      01-FEB-2001 (first entry)
DE
XX      PR-39 peptide used in angiogenesis control.
XX      Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;
KW      myocardial ischaemia; proteasome.
XX
XX      Synthetic.
OS
XX      WO200057895-A1.
XX
XX      05-OCT-2000.
XX
XX      16-MAR-2000; 2000WO-US007050.
XX
XX      26-MAR-1999; 99US-00276868.
XX
XX      (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX      Simons M, Gao Y;
XX
XX      WPI; 2000-628319/60.
XX
XX      Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
XX      infarction, by administering a PR-39 oligopeptide that regulates
XX      enzymatic activity of proteasomes.
XX
XX      Disclosure; Page 21; 51pp; English.
XX
XX      This invention relates to a method for the stimulation of angiogenesis in
XX      situ within a targeted collection of viable cells. The method comprises
XX      introducing, into the cytoplasm, at least 1 member of the PR-39
XX      oligopeptide collective, which interacts with cytoplasmic proteasomes.
XX      Part of the proteolytic activity of the proteasomes is selectively
XX      altered so as to stimulate angiogenesis. The method is used to induce
XX      angiogenesis in tissue that has suffered anoxia or infarction, e.g.
XX      myocardial infarction or chronic myocardial ischaemia, and also to study
XX      the mechanisms that control angiogenesis. The present sequence represents
XX      the PR-39 peptide from which peptide used in the method of the invention

```

CC are derived  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 155; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26  
| | | | | | | | | | | | | | | | | | | |  
Db 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26

RESULT 11  
AAB97280  
ID AAB97280 standard; peptide; 39 AA.  
XX  
AC AAB97280;  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE PR-39 peptide.  
XX  
KW PR-39; cathelin; inflammation; wound healing; myocardial infarction;  
KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;  
KW anoxia; chronic myocardial ischaemia; heart tissue.  
XX  
OS Unidentified.  
XX  
PN WO200130368-A1.  
XX  
PD 03-MAY-2001.  
XX  
PF 06-OCT-2000; 2000WO-US027552.  
XX  
PR 25-OCT-1999; 99US-00426011.  
XX  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Simons M, Gao Y;  
XX  
DR WPI; 2001-355179/37.  
XX  
PT Stimulation of angiogenesis and inhibition of proteasome mediated  
PT degradation in cells, by introduction of PR-39 oligopeptide or its N-  
PT terminal fragments or their conjugates, for use in anoxia and infarction  
PT conditions.  
XX  
PS Disclosure; Page 21; 52pp; English.  
XX  
CC Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39  
CC is a member of the the cathelin family of proteins, mature PR-39  
CC represented by the present sequence is 39 amino acids in length, and has  
CC been shown to play a role in several inflammatory events including wound  
CC healing and myocardial infarction. The PR-39 derived family of  
CC oligopeptides cause selective inhibition of proteasome mediated  
CC degeneration of peptides and stimulation of angiogenesis after their  
CC intracellular introduction to a target cell. PR-39 derived peptides are  
CC able to interact with at least the alpha7 subunit of the proteasomes, and  
CC therefore alter the proteolytic activity of proteasomes such that a  
CC selective increased expression of specific proteins occurs. The invention  
CC includes methods for the selective inhibition of proteasome mediated  
CC peptide degradation. The method provides means for stimulating  
CC angiogenesis as required in living tissues and organs which have suffered  
CC defects or have undergone anoxia and/or infarction, myocardial infarction  
CC or chronic myocardial ischaemia of heart tissue. Examples are the  
CC myocardium, skeletal or smooth muscle, artery or vein, lung, brain,  
CC kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and  
CC extremities. A particular example is after myocardial infarction or  
CC ischaemia  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 155; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26  
| | | | | | | | | | | | | | | | | | | |  
Db 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26

RESULT 12  
AAB84690  
ID AAB84690 standard; protein; 39 AA.  
XX  
AC AAB84690;  
XX  
DT 17-SEP-2001 (first entry)  
XX  
DE Amino acid sequence of a PR-39 protein.  
XX  
KW PR-39; IkappaBalpa degradation; NfkappaB transcription factor;  
KW myocardial infarction; chronic myocardial ischemia; heart disease;  
KW anoxia.  
XX  
OS Unidentified.  
XX  
PN WO200147540-A1.  
XX  
PD 05-JUL-2001.  
XX  
PF 27-DEC-2000; 2000WO-US035293.  
XX  
PR 29-DEC-1999; 99US-00474967.  
XX  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Simons M, Gao Y;  
XX  
DR WPI; 2001-441690/47.  
XX  
PT Selective inhibition of IkappaBalpa degradation within targeted viable  
PT cell collection, involves interacting PR-39 oligopeptide with  
PT IkappaBalpa and proteasomes, and altering proteolytic activity of  
PT proteasomes.  
XX  
PS Disclosure; Page 30; 69pp; English.  
XX  
CC The present sequence represents a PR-39 protein. The specification  
CC describes PR-39 derived peptides, which are used for selective inhibition  
CC of IkappaBalpa degradation within a targeted cell collection in-situ.  
CC The method is useful for selectively inhibiting IkappaBalpa protein  
CC degradation in situ, decreasing the activity of NfkappaB transcription  
CC factor and selective control of NfkappaB-dependent gene expression in  
CC situ. The PR-39 derived peptides are useful in the treatment of  
CC myocardial infarction, chronic myocardial ischemia of heart disease and  
CC anoxia  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 155; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26  
| | | | | | | | | | | | | | | | | | | |  
Db 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26

RESULT 13  
ADD35364  
ID ADD35364 standard; peptide; 39 AA.  
XX  
AC ADD35364;  
XX



DT 15-JAN-2004 (first entry)  
XX Antimicrobial peptide PR-39.  
DE antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological;  
XX intraocular pressure; glaucoma; ocular hypertension; hyperaemia;  
KW irritation; inflammation; conjunctiva; ocular cell dysplasia;  
KW iridial melanocyte hyperplasia; hyperpigmentation.  
XX Unidentified.  
OS WO2003079997-A2.  
XX PN 02-OCT-2003.  
XX PD 21-MAR-2003; 2003WO-US008935.  
XX PF 21-MAR-2002; 2002US-0367071P.  
XX PR (CAYM-) CAYMAN CHEM CO.  
XX PA Maxey KM, Johnson J;  
XX PI WPI; 2004-011506/01.  
XX DR Ophthalmic solution useful for the treatment of increased intraocular  
XX PT pressure comprises a prostaglandin of the F-series and an antimicrobial  
XX PT peptide.  
XX PS Disclosure; Page 11; 11pp; English.  
XX CC The invention relates to a novel ophthalmic solution comprising a  
CC prostaglandin of the F-series and an antimicrobial peptide. A solution of  
CC the invention has hypotensive and ophthalmological activity. The solution  
CC is useful for the treatment of increased intraocular pressure, such as  
CC caused by glaucoma and for the reduction of ocular hypertension. The  
CC prostaglandin and the antimicrobial peptide work synergistically, to  
CC provide beneficial reduction in the incidence of irritant and toxic side  
CC effects such as hyperaemia, irritation and inflammation of conjunctiva,  
CC ocular cell dysplasia, iridial melanocyte hyperplasia, and  
CC hyperpigmentation, associated with the prior art prostaglandin  
CC compositions. The present sequence represents an antimicrobial peptide of  
CC the invention.  
XX SQ Sequence 39 AA;  
Query Match 100.0%; Score 155; DB 8; Length 39;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRRPPPPFFPPRLPPRI 26  
Db 1 RRRPRPPYLP RRRPPPPFFPPRLPPRI 26  
RESULT 14  
ADE86112  
ID ADE86112 standard; peptide; 39 AA.  
XX AC ADE86112;  
XX DT 29-JAN-2004 (first entry)  
XX DE Proline-arginine (PR)-rich antimicrobial peptide PR-39.  
KW Leukocyte superoxide anion; leukocyte O2- production;  
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;  
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;  
KW tissue damage; oxygen radical; antibacterial.  
XX OS Synthetic.  
XX PN US2003125249-A1.

DT 03-JUL-2003.  
XX PD  
XX PF 07-DEC-2001; 2001US-00014147.  
XX PR 10-APR-1995; 95US-00419066.  
XX PR 08-OCT-1997; 97US-00930777.  
XX PA (BLEC/) BLECHA-F.  
XX PA (SHIJ/) SHI J.  
XX PI Blecha F, Shi J;  
XX PI WPI; 2004-059188/06.  
XX DR  
XX PT Attracting leukocyte to location by administering peptide including  
XX PT proline-arginine-rich antimicrobial peptide or its truncated analogs to  
XX PT the location.  
XX PS Claim 2; SEQ ID NO 1; 24pp; English.  
XX CC The present invention relates to a method of inhibiting leukocyte  
CC superoxide anion (O2-) production and/or attracting leukocytes. The  
CC method comprises the use of proline-arginine (PR)-rich antimicrobial  
CC peptides or their truncated analogues. The method is useful for  
CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or  
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are  
CC useful as medicaments to fight infection by attracting leukocytes to a  
CC wound site, while restricting tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leukocytes. The present  
CC sequence represents a PR-rich antimicrobial peptide.  
XX SQ Sequence 39 AA;  
Query Match 100.0%; Score 155; DB 8; Length 39;  
Best Local Similarity 100.0%; Pred. No. 7.2e-09;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRRPPPPFFPPRLPPRI 26  
Db 1 RRRPRPPYLP RRRPPPPFFPPRLPPRI 26  
RESULT 15  
ADL67254  
ID ADL67254 standard; peptide; 39 AA.  
XX AC ADL67254;  
XX DT 20-MAY-2004 (first entry)  
XX DE Antimicrobial peptide PR-39.  
XX KW Leucocyte ; superoxide anion; oxygen radical; proline-arginine ;  
KW antimicrobial; antioxidant; NADPH oxidase ; p47phox; neutrophil;  
KW infection; wound ; tissue damage ; PR-39 peptide.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
FT Peptide 1. .26 /label= PR-26\_peptide  
FT Peptide 1. .19 /label= PR-19\_peptide  
FT Peptide 1. .14 /label= PR-14\_peptide  
FT Region 1. .3 /note= "Essential for antibacterial activity"  
FT Peptide 4. .26 /label= PR-23\_peptide  
FT Peptide 11. .26 /label= PR-16\_peptide  
FT Region 20. .26





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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 19.3818 Seconds  
(without alignments)  
129.071 Million cell updates/sec

Title: US-10-014-147-2  
Perfect score: 155  
Sequence: 1 RRRPRPYLPRRPPPPFPRLPPI 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	100.0	172	2 S68232	antimicrobial prot
2	84.5	54.5	301	2 JQ1663	hybrid proline-ric
3	82	52.9	59	2 A36589	bactenecin 7 - bov
4	80	51.6	199	2 S14981	extensin class I (
5	78	50.3	278	2 A49266	fas ligand - rat
6	77	49.7	281	2 I38707	Fas ligand - human
7	75.5	48.7	1029	2 T30351	mucin-like protein
8	75	48.4	1006	2 G86292	hypothetical prote
9	74.5	48.1	212	2 S57330	cathelin-like anti
10	73.5	47.4	1460	1 EDBEIF	immediate-early pr
11	73	47.1	439	2 S51939	chitinase (EC 3.2.
12	72	46.5	415	1 A34170	acrosin (EC 3.4.21
13	71.5	46.1	42	2 B36589	bactenecin 5 - bov
14	71.5	46.1	176	2 A45328	bactenecin 5 precu
15	71.5	46.1	1958	2 B40505	hypothetical prote
16	70	45.2	389	2 S27200	proline-rich prote
17	70	45.2	2871	2 A55624	fibrillin-1 precur
18	69.5	44.8	221	2 T07176	extensin homolog -
19	69.5	44.8	228	2 S40463	prophenin (PR-2) p
20	69.5	44.8	491	2 T07598	proline-rich prote
21	69	44.5	254	2 T25073	hypothetical prote
22	69	44.5	296	2 A27319	gliadin - wheat
23	69	44.5	296	2 S07361	saliva/beta-gliadin
24	68.5	44.2	57	2 S10782	salivary protein P
25	68.5	44.2	79	1 PJHUSB	proline-rich pepti
26	68	43.9	134	2 JC5572	proline-rich prote
27	68	43.9	190	2 S68230	antimicrobial pept
28	68	43.9	239	2 T16159	hypothetical prote
29	68	43.9	588	2 T45564	hypothetical prote

30	68	43.9	903	2 T00074	hypothetical prote
31	67.5	43.5	82	2 A41051	spore coat protein
32	67.5	43.5	134	2 D84672	hypothetical prote
33	67.5	43.5	148	2 S39206	proline-rich prote
34	67.5	43.5	428	2 E71415	probable coll wall
35	67.5	43.5	547	2 C96828	unknown protein F1
36	67	43.2	209	2 A48232	cysteine-rich exte
37	67	43.2	359	2 T13478	hypothetical prote
38	67	43.2	381	2 S52985	cell wall protein
39	67	43.2	1098	2 T08599	probable transcrip
40	66.5	42.9	299	2 T09792	proline-rich prote
41	66.5	42.9	508	2 T45867	hypothetical prote
42	66	42.6	147	2 S37485	gene mag1 protein
43	66	42.6	246	2 T46446	hypothetical prote
44	66	42.6	251	1 B60492	homeotic protein H
45	66	42.6	424	2 A54964	spliceosome-associ

ALIGNMENTS

RESULT 1

S68232  
antimicrobial protein PR-39 precursor, cathelin-associated - pig  
N/Alternate names: myeloid antibacterial protein PR-39  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S68232; JN0899; I47138; S19563  
R/Zhao, C.; Ganz, T.; Lehrer, R.I.  
FEBS Lett. 376, 130-134, 1995  
A/Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen  
A/Reference number: S68232; MUID:96105365; PMID:7498526  
A/Accession: S68232  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-172 <ZHA>  
A/Cross-references: UNIPROT:P80054; EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g116  
A/Experimental source: leukocytes  
R/Storici, P.; Zanetti, M.  
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993  
A/Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i  
A/Reference number: JN0899; MUID:94071853; PMID:8250863  
A/Accession: JN0899  
A/Molecule type: mRNA  
A/Residues: 1-20,'A',22-172 <STO>  
A/Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101  
A/Experimental source: bone marrow cells  
R/Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bome  
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995  
A/Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami  
A/Reference number: I47138; MUID:95350216; PMID:7624374  
A/Accession: I47138  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-28,'T',30-89,'QR',92-116,'NDP',120-172 <GUD>  
A/Cross-references: EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PID:g1051298  
R/Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,  
Eur. J. Biochem. 202, 849-854, 1991  
A/Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of th  
A/Reference number: S19563; MUID:92111534; PMID:1765098  
A/Accession: S19563  
A/Molecule type: protein  
A/Residues: 131-169 <AGE>  
A/Experimental source: intestine  
C/Genetics:  
A/Gene: PR39  
A/Introns: 66/3; 102/3; 126/3  
C/Superfamily: cathelin; cystatin homolog  
C/Keywords: amidated carboxyl end; antibacterial  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;22-129/Domain: cystatin homolog <CYS>  
F;30-130/Domain: propeptide #status predicted <PRO>  
F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

F:169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 100.0%; Score 155; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 6e-09;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLRRPRPPPPFFPPRLPPRI 26  
| | | | | | | | | | | | | | | | | | | | | |  
Db 131 RRRPRPPYLRRPRPPPPFFPPRLPPRI 156

RESULT 2  
JQ1663  
hybrid proline-rich protein - maize  
C:Species: Zea mays (maize)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: JQ1663  
R;Jose-Estanyol, M.; Ruiz-Avila, L.; Puigdomenech, P.  
Plant Cell 4, 413-423, 1992  
A:Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein.  
A:Reference number: JQ1663; MUID:92361259; PMID:1498600  
A:Accession: JQ1663  
A:Molecule type: DNA  
A:Residues: 1-301 <JOS>  
A:Cross-references: UNIPROT:Q41848; EMBL:X60432; NID:g433706; PIDN:CAA42959.1; PID:g4337  
A:Experimental source: strain W64A  
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 54.5%; Score 84.5; DB 2; Length 301;  
Best Local Similarity 58.3%; Pred. No. 0.092;  
Matches 14; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 4 PRPPYL---PRPRPPPPFFPPRLPP 24  
| | | | | | | | | | | | | | | | | | | | | |  
Db 169 PTPPYVPTTRPRSPPPYVPPYVPP 192

RESULT 3  
A36589  
bactenecin 7 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-May-1997  
C:Accession: A36589  
R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.  
J. Biol. Chem. 265, 18871-18874, 1990  
A:Title: Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of  
A:Reference number: A36589; MUID:91035404; PMID:2229048  
A:Accession: A36589  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-59 <FRA>  
C:Superfamily: cathelin; cystatin homology

Query Match 52.9%; Score 82; DB 2; Length 59;  
Best Local Similarity 68.0%; Pred. No. 0.035;  
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 RRRPRPPYLRRPRPPPPFFPPRLPPR 25  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 RIRPRPRLRRPRRPLPFPRPGPR 26

RESULT 4  
S14981  
extensin class I (clone wl-8 L) - tomato (fragment)  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 11-Jan-2000  
C:Accession: S14981  
R;Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.  
Plant Mol. Biol. 16, 547-565, 1991  
A:Title: Tomato extensin and extensin-like cDNAs: structure and expression in response t  
A:Reference number: S14970; MUID:91329690; PMID:1714316  
A:Accession: S14981

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-199 <SHO>  
A:Cross-references: EMBL:X55692  
A:Experimental source: cv. UC82B  
C:Superfamily: hydroxyproline-rich glycoprotein  
C:Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 51.6%; Score 80; DB 2; Length 199;  
Best Local Similarity 60.9%; Pred. No. 0.17;  
Matches 14; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 RRRPRPPYLRRPRPPPPFFPPRLPP 24  
| | | | | | | | | | | | | | | | | | | | | |  
Db 69 RPRPPPPPPRPPPEYLPPLPP 91

RESULT 5  
A49266  
fas ligand - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: A49266  
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.  
Cell 75, 1169-1178, 1993  
A:Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor  
A:Reference number: A49266; MUID:94084792; PMID:7505205  
A:Accession: A49266  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-278 <SUD>  
A:Cross-references: UNIPROT:P36940; GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179  
C:Keywords: glycoprotein; transmembrane protein

Query Match 50.3%; Score 78; DB 2; Length 278;  
Best Local Similarity 62.5%; Pred. No. 0.37;  
Matches 15; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 RRRPRPPYLRRPRPPPPFFPPRLPP 24  
| | | | | | | | | | | | | | | | | | | | | |  
Db 43 RPRPPPPPPSPLPPSQPPPLPP 66

RESULT 6  
I38707  
Fas ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C:Accession: I38707; JC2340; S57565; I38554  
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.  
Int. Immunol. 6, 1567-1574, 1994  
A:Title: Human Fas ligand: gene structure, chromosomal location and species specificity.  
A:Reference number: I38707; MUID:95127560; PMID:7826947  
A:Accession: I38707  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-281 <RES>  
A:Cross-references: UNIPROT:P48023; EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g59543  
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.;  
Biochem. Biophys. Res. Commun. 204, 468-474, 1994  
A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.  
A:Reference number: JC2340; MUID:95071350; PMID:7980502  
A:Accession: JC2340  
A:Molecule type: DNA  
A:Residues: 1-281 <MIT>  
A:Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:gl369902  
R;Schatzlein, C.E.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: S57565  
A:Accession: S57565  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-281 <SCH>

Db 156 RQRPGPPAAPGARPPP-QPFRPPP 178



RESULT 11  
S51939  
Chitinase (EC 3.2.1.14) precursor - beet  
C:Species: Beta vulgaris (beet)  
C:Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: S51939; S72315; S45025  
R;Berglund, L.; Brunstedt, J.; Nielsen, K.K.; Chen, Z.; Mikkelsen, J.D.; Marcker, K.A.  
Plant Mol. Biol. 27, 211-216, 1995  
A:Title: A proline-rich chitinase from Beta vulgaris.  
A:Reference number: S51939; MUID:95170004; PMID:7865792  
A:Accession: S51939  
A:Molecule type: DNA  
A:Residues: 1-439 <BER>  
A:Cross-references: UNIPROT:Q42421; EMBL:X79301; NID:g488730; PID:g488731  
A:Note: the authors translated the codon TGC for residue 416 as Gly  
A:Accession: S72315  
A:Molecule type: mRNA  
A:Residues: 191-397 <BER2>  
C:Genetics:  
A:Introns: 248/1; 300/2  
C:Keywords: glycosidase; hydrolase  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-439/Product: chitinase #status predicted <MAT>  
F;183-423/Domain: plant chitinase homology <PCH>  
  
Query Match 47.1%; Score 73; DB 2; Length 439;  
Best Local Similarity 66.7%; Pred. No. 1.8;  
Matches 14; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 4 PRPPYLPRLPPPPPPRLPP 24  
Db 114 PRPPPPTPRPPPPPTPRPP 134  
  
RESULT 12  
A34170  
acrosin (EC 3.4.21.10) precursor - pig  
N;Alternate names: S3K fucose-binding protein  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A34170; S08994; S02428; S04940; S16657; S02780; S10695; S12968  
R;Baba, T.; Kashiwabara, S.; Watanabe, K.; Itoh, H.; Michikawa, Y.; Kimura, K.; Takada, J. Biol. Chem. 264, 11920-11927, 1989  
A:Title: Activation and maturation mechanisms of boar acrosin zymogen based on the deduction of the structure of the matured enzyme.  
A:Reference number: A34170; MUID:89308595; PMID:2745422  
A:Accession: A34170  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-415 <BAB>  
A:Cross-references: UNIPROT:P08001; GB:J04950; NID:g164702; PIDN:AAA31131.1; PID:g164703  
R;Cechova, D.; Toepfer-Petersen, E.; Zucker, A.; Jonakova, V.  
Biol. Chem. Hoppe-Seyler 371, 317-323, 1990  
A:Title: Is sperminogen a modified proacrosin? Isolation, purification, and partial characterization of the matured enzyme.  
A:Reference number: S08994; MUID:90253655; PMID:2111146  
A:Accession: S08994  
A:Molecule type: protein  
A:Residues: 'X',18,'X',20-25,'X',27-32,'X',34-38,'X',40-50 <CEC>  
R;Toepfer-Petersen, E.; Henschen, A.  
FEBS Lett. 226, 38-42, 1987  
A:Title: Acrosin shows zona and fucose binding, novel properties for a serine proteinase  
A:Reference number: S02428; MUID:88083633; PMID:3480243  
A:Accession: S02428  
A:Molecule type: protein  
A:Residues: 17-32;40-55 <TOE>  
R;Adham, I.M.; Klemm, U.; Maier, W.M.; Hoyer-Fender, S.; Tsaousidou, S.; Engel, W.  
Eur. J. Biochem. 182, 563-568, 1989  
A:Title: Molecular cloning of preproacrosin and analysis of its expression pattern in spermatozoa.  
A:Reference number: S04940; MUID:89325301; PMID:2502391  
A:Accession: S04940  
A:Molecule type: mRNA  
A:Residues: 1-7,9-210,'Q',212-216,'VT',219-346,'A',348-388,390-393,'GN',396,'LVE',399-400  
A:Cross-references: EMBL:X14844

A:Note: the authors translated the codon CCT for residue 240 as Ala, GCC for residue 264  
R;Adham, I.M.  
submitted to the EMBL Data Library, March 1989  
A:Reference number: S16657  
A:Accession: S16657  
A:Molecule type: mRNA  
A:Residues: 1-7,9-210,'Q',212-216,'VT',219-346,'A',348-388,390-398,'KELL', <AD2>  
A:Cross-references: EMBL:X14844; NID:g1867; PIDN:CAA32948.1; PID:g1868  
A:Note: the difference at the carboxyl end is due to a frameshift error  
R;Baba, T.; Michikawa, Y.; Kawakura, K.; Arai, Y.  
FEBS Lett. 244, 132-136, 1989  
A:Title: Activation of boar proacrosin is effected by processing at both N- and C-terminal  
A:Reference number: S02780; MUID:89171246; PMID:2494060  
A:Accession: S02780  
A:Molecule type: protein  
A:Residues: 17-69 <BA2>  
R;Toepfer-Petersen, E.; Steinberger, M.; von Eschenbach, C.E.; Zucker, A.  
FEBS Lett. 265, 51-54, 1990  
A:Title: Zona pellucida-binding of boar sperm acrosin is associated with the N-terminal  
A:Reference number: S10695; MUID:90306316; PMID:2365054  
A:Accession: S10695  
A:Molecule type: protein  
A:Residues: 40-62 <TO2>  
R;Toepfer-Petersen, E.; Calvete, J.; Schaefer, W.; Henschen, A.  
FEBS Lett. 275, 139-142, 1990  
A:Title: Complete localization of the disulfide bridges and glycosylation sites in boar sperm acrosin  
A:Reference number: S12968; MUID:91085546; PMID:2261983  
A:Accession: S12968  
A:Molecule type: protein  
A:Residues: 17-29;34-66;68-91;94-121,123-166;171-184;190-207;209-216;219-228;231-245;248-250  
C:Superfamily: acrosin; trypsin homology  
C:Keywords: glycoprotein; hydrolase; serine proteinase; sperm  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-415/Product: acrosin #status experimental <MAT>  
F;17-39/Product: acrosin light (A) chain #status experimental <LCH>  
F;40-415/Product: acrosin heavy (B) chain #status experimental <HCH>  
F;40-283/Domain: trypsin homology <TRY>  
F;300-374/Region: proline-rich  
F;19,208/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;22-152,26-160,71-87,175-244,207-223,234-264/Disulfide bonds: #status experimental  
F;86,140,238/Active site: His, Asp, Ser #status predicted  
  
Query Match 46.5%; Score 72; DB 1; Length 415;  
Best Local Similarity 63.6%; Pred. No. 2.1;  
Matches 14; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 3 RRPYPYLPRLPPPPPPRLPP 24  
Db 338 RRPYPAPPPPPPPPPPPPPPP 359  
  
RESULT 13  
B36589  
bactenecin 5 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 08-Dec-1995  
C:Accession: B36589  
R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.  
J. Biol. Chem. 265, 18871-18874, 1990  
A:Title: Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of bovine neutrophils.  
A:Reference number: A36589; MUID:91035404; PMID:2229048  
A:Accession: B36589  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-42 <FRA>  
C:Superfamily: cathelin; cystatin homology  
  
Query Match 46.1%; Score 71.5; DB 2; Length 42;  
Best Local Similarity 57.1%; Pred. No. 0.28;  
Matches 16; Conservative 1; Mismatches 6; Indels 5; Gaps 2;  
  
Qy 2 RRP--RPPYLPRLPP--PPPPFRLPP 24  
Db 114 RPPPPPPTPRPPPPPTPRPP 134



Db 7 RRPPIRPPFYPPFRPPPIRPPPIRPP 34

RESULT 14

A45328

bactenecin 5 precursor - bovine

N;Alternate names: Bac5; neutrophil antibiotic protein 5

C;Species: Bos primigenius taurus (cattle)

C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004

C;Accession: A45328

R;Zanetti, M.; Del Sal, G.; Storici, P.; Schneider, C.; Roméo, D.

J. Biol. Chem. 268, 522-526, 1993

A;Title: The cDNA of the neutrophil antibiotic Bac5 predicts a pro-sequence homologous b

A;Reference number: A45328; MUID:93107055; PMID:8416958

A;Accession: A45328

A;Molecule type: mRNA

A;Residues: 1-176 <ZAN>

A;Cross-references: UNIPROT:P19660; GB:L02650; NID:g162730; PIDN:AAA30404.1; PID:g162731

A;Note: sequence extracted from NCBI backbone (NCBIP:121443)

C;Superfamily: cathelin; cystatin homology

C;Keywords: amidated carboxyl end; antibacterial

F;1-29/Domain: signal sequence #status predicted <SIG>

F;22-129/Domain: cystatin homology <CYS>

F;30-130/Domain: propeptide #status predicted <PRO>

F;131-173/Product: neutrophil antibiotic protein Bac5 #status predicted <MAT>

F;173/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 46.1%; Score 71.5; DB 2; Length 176;

Best Local Similarity 57.1%; Pred. No. 1.1;

Matches 16; Conservative 1; Mismatches 6; Indels 5; Gaps 2;

QY 2 RRP--RPPYLPRRP---PPFFPPRLPP 24

Db 137 RRPPIRPPFYPPFRPPPIRPPPIRPP 164

RESULT 15

B40505

hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhuser or Becker)

C;Species: suid herpesvirus 1

C;Date: 10-Apr-1992 #sequence\_revision 10-Apr-1992 #text\_change 09-Jul-2004

C;Accession: B40505

R;Cheung, A.K.

J. Virol. 65, 5260-5271, 1991

A;Title: Cloning of the latency gene and the early protein 0 gene of pseudorabies virus.

A;Reference number: A40505; MUID:91374576; PMID:1654441

A;Accession: B40505

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1958 <CHE>

A;Cross-references: UNIPROT:Q69340; GB:M57505; NID:g334066; PIDN:AAA47468.1; PID:g334068

C;Superfamily: pseudorabies virus 1 nuclear antigen

Query Match 46.1%; Score 71.5; DB 2; Length 1958;

Best Local Similarity 62.5%; Pred. No. 10;

Matches 15; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 RRRPPPYLPRPPPPFFPPRLPP 24

Db 477 RDDPRPP-SPPRPPPPPLPPPPPP 499

Search completed: October 26, 2005; 05:19:58

Job time : 20.3818 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:52:03 ; Search time 90.0546 Seconds  
(without alignments)  
147.844 Million cell updates/sec

Title: US-10-014-147-2  
Perfect score: 155  
Sequence: 1 RRRPRPPYLPRPRPPPPFFPRLPPRI 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	155	100.0	172	1	PR39_PIG	P80054 sus scrofa
2	85.5	55.2	228	2	Q6Z8Z0	Q6z8z0 oryza sativ
3	84.5	54.5	301	2	Q41848	Q41848 zea mays (m
4	82	52.9	190	1	BCT7_BOVIN	P19661 bos taurus
5	81	52.3	514	2	Q6QFF1	Q6qtf1 arabidopsis
6	81	52.3	520	2	Q9LV14	Q9lv14 arabidopsis
7	79	51.0	333	2	Q9XI23	Q9xi23 oryza sativ
8	78	50.3	278	1	TNF6_RAT	P36940 rattus norv
9	77.5	50.0	625	2	Q8S9B5	Q8s9b5 volvox cart
10	77	49.7	281	1	TNF6_HUMAN	P48023 homo sapien
11	77	49.7	1395	2	Q7SC01	Q7sc01 neurospora
12	76.5	49.4	185	2	Q94JF6	Q94jfe oryza sativ
13	76	49.0	183	2	Q94J98	Q94j98 oryza sativ
14	76	49.0	409	2	Q9SBM1	Q9sbm1 volvox cart
15	75.5	48.7	1029	2	Q9YMX0	Q9ymx0 lymantria d
16	75	48.4	1006	2	Q9LMO1	Q9lmq1 arabidopsis
17	74.5	48.1	212	1	PF11_PIG	P51524 sus scrofa
18	74.5	48.1	342	2	Q6ZD62	Q6zdd62 oryza sativ
19	74.5	48.1	816	2	Q7Q3J9	Q7q3j9 anopheles g
20	74	47.7	1134	2	Q96JH1	Q96jhi homo sapien
21	73	47.1	439	2	Q42421	Q42421 beta vulgar
22	73	47.1	548	2	Q6ESK7	Q6esk7 oryza sativ
23	72.5	46.8	236	2	Q657Y0	Q657y0 oryza sativ
24	72.5	46.8	480	2	Q740X0	Q740x0 mycobacteri
25	72	46.5	147	2	Q6F392	Q6f392 oryza sativ
26	72	46.5	415	1	ACRO_PIG	P08001 sus scrofa
27	72	46.5	1200	2	Q96PN7	Q96pn7 homo sapien
28	72	46.5	2374	2	Q7SBD3	Q7sbd3 neurospora
29	71.5	46.1	176	1	BCT5_BOVIN	P19660 bos taurus
30	71.5	46.1	591	2	P79817	P79817 oryzias lat
31	71.5	46.1	666	2	Q8JHT8	Q8jht8 oryzias lat

32	71.5	46.1	670	2	Q8JI22	Q8ji22 oryzias lat
33	71.5	46.1	1958	2	Q69340	Q69340 suid herpes
34	71	45.8	103	2	Q99FW9	Q99fw9 human papil
35	71	45.8	687	2	Q948Y7	Q948y7 volvox cart
36	70.5	45.5	146	2	Q7Q8P5	Q7q8p5 anopheles g
37	70.5	45.5	206	2	Q74C95	Q74c95 geobacter s
38	70.5	45.5	210	2	Q6ZJEG	Q6zje9 oryza sativ
39	70.5	45.5	280	1	TNF6_CERTO	Q9bdn1 cercocebus
40	70.5	45.5	782	1	SX30_MOUSE	Q8cgv4 mus musculu
41	70.5	45.5	3409	2	Q6SS6E	Q6sse6 chlamydomon
42	70	45.2	273	2	Q82PZ6	Q82pz6 streptomyce
43	70	45.2	366	2	Q84X72	Q84x72 chlamydomon
44	70	45.2	401	2	Q8S054	Q8s054 oryza sativ
45	70	45.2	605	2	Q9Q5L3	Q9q5l3 cercopithec

ALIGNMENTS

RESULT 1

ID	PR39_PIG	STANDARD;	PRT;	172 AA.
AC	P80054; Q9TR84;			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Antibacterial protein PR-39 precursor.			
GN	Name=PR39;			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95350216; PubMed=7624374;			
RA	Gudmundsson G.H.; Magnusson K.P.; Chowdhary B.P.; Johansson M.,			
RA	Andersson L.; Boman H.G.;			
RT	"Structure of the gene for porcine peptide antibiotic PR-39, a			
RT	cathelin gene family member: comparative mapping of the locus for the			
RT	human peptide antibiotic FALL-39.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=94071853; PubMed=8250863;			
RA	Storici P.; Zanetti M.;			
RT	"A cDNA derived from pig bone marrow cells predicts a sequence			
RT	identical to the intestinal antibacterial peptide PR-39.";			
RL	Biochem. Biophys. Res. Commun. 196:1058-1065(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;			
RA	Zhao C.; Ganz T.; Lehrer R.I.;			
RT	"Structures of genes for two cathelin-associated antimicrobial			
RT	peptides: prophenin-2 and PR-39.";			
RL	FEBS Lett. 376:130-134(1995).			
RN	[4]			
RP	SEQUENCE OF 131-169.			
RC	TISSUE=Intestine;			
RX	MEDLINE=92111534; PubMed=1765098;			
RA	Agerberth B.; Lee J.-Y.; Bergman T.; Carlquist M.; Boman H.G.,			
RA	Mutt V.; Joernvall H.;			
RT	"Amino acid sequence of PR-39. Isolation from pig intestine of a new			
RT	member of the family of proline-arginine-rich antibacterial			
RT	peptides.";			
RL	Eur. J. Biochem. 202:849-854(1991).			
RN	[5]			
RP	SEQUENCE OF 131-164, AND FUNCTION.			
RC	TISSUE=Neutrophils;			
RX	MEDLINE=95088504; PubMed=7996056;			
RA	Shi J.; Ross C.R.; Chengappa M.M.; Blecha F.;			
RT	"Identification of a proline-arginine-rich antibacterial peptide from			

RT neutrophils that is analogous to PR-39, an antibacterial peptide from  
RT the small intestine.";  
RL J. Leukoc. Biol. 56:807-811(1994).  
CC -!- FUNCTION: Exerts a potent antimicrobial activity against both  
CC E.coli and B.megaterium.  
CC -!- TISSUE SPECIFICITY: Small intestine and bone marrow.  
CC -!- SIMILARITY: Belongs to the cathelicidin family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; X87236; CAA0682.1; -.  
DR EMBL; L23825; AAA31109.1; -.  
DR EMBL; X89201; CAA61487.1; -.  
DR PIR; S68232; S68232.  
DR HSSP; P32196; 1KWI.  
DR InterPro; IPR001894; Cathelicidin.  
DR Pfam; PF00666; Cathelicidins; 1.  
DR ProDom; PD001838; Cathelicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
KW Amidation; Antibiotic; Direct protein sequencing;  
KW Pyrrolidone carboxylic acid; Signal.  
FT SIGNAL 1 29 Potential.  
FT PROPEP 30 130  
FT CHAIN 131 169 Antibacterial protein PR-39.  
FT MOD\_RES 30 30 Pyrrolidone carboxylic acid (By  
FT similarity).  
FT DISULFID 85 96 By similarity.  
FT DISULFID 107 124 By similarity.  
FT MOD\_RES 169 169 proline amide (G-170 provides amide  
FT group).  
FT CONFLICT 21 21 G -> A (in Ref. 2).  
FT CONFLICT 29 29 A -> T (in Ref. 1).  
FT CONFLICT 90 91 RQ -> QR (in Ref. 1).  
FT CONFLICT 117 119 IHS -> NDP (in Ref. 1).  
FT CONFLICT 157 157 P -> I (in Ref. 5).  
SQ SEQUENCE 172 AA; 19476 MW; 994B792798C0E133 CRC64;  
  
Query Match 100.0%; Score 155; DB 1; Length 172;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRRPRPPYLPRPPPPFFPPRLPPRI 26  
Db 131 RRRPRPPYLPRPPPPFFPPRLPPRI 156  
  
RESULT 2  
Q6Z8Z0 ID Q6Z8Z0 PRELIMINARY; PRT; 228 AA.  
AC Q6Z8Z0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein P0501G04.17.  
GN Name=P0501G04.17;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP004752; BAD07841.1; -.  
KW Hypothetical protein.

SQ SEQUENCE 228 AA; 24277 MW; EACA08812E410106 CRC64;  
  
Query Match 55.2%; Score 85.5; DB 2; Length 228;  
Best Local Similarity 55.2%; Pred. No. 0.58;  
Matches 16; Conservative 3; Mismatches 5; Indels 5; Gaps 1;  
  
QY 2 RRRPRPY-----LPRPRPPPPFFPPRLPPR 25  
Db 21 RRORPPWSASHRLPKPHPPPTWSPRP 49  
  
RESULT 3  
Q41848 ID Q41848 PRELIMINARY; PRT; 301 AA.  
AC Q41848;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Prolin rich protein.  
GN Name=PRP;  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W64A;  
RX MEDLINE=92361259; PubMed=1498600;  
RA Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;  
RT "A maize embryo-specific gene encodes a proline-rich and hydrophobic  
RT protein.";  
RL Plant Cell 4:413-423(1992).  
DR EMBL; X60432; CAA42959.1; -.  
DR PIR; JQ1663; JQ1663.  
DR HSSP; P24337; 1HYP.  
DR InterPro; IPR003612; AAI.  
DR Pfam; PF00234; Tryp\_alpha\_amyl; 1.  
DR SMART; SM00499; AAI; 1.  
SQ SEQUENCE 301 AA; 31647 MW; 884EB70854D28C2E CRC64;  
  
Query Match 54.5%; Score 84.5; DB 2; Length 301;  
Best Local Similarity 58.3%; Pred. No. 0.95;  
Matches 14; Conservative 3; Mismatches 4; Indels 3; Gaps 1;  
  
QY 4 PRPPYL--PRPRPPPPFFPPRLPP 24  
Db 169 FTTPPVVPTPRSPPPYPVPYVPP 192  
  
RESULT 4  
BCT7 BOVIN ID BCT7 BOVIN STANDARD; PRT; 190 AA.  
AC P19661;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bactenecin 7 precursor (BAC7) (PR-59).  
GN Name=BAC7;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=95010707; PubMed=7925973; DOI=10.1016/0014-5793(94)00954-6;  
RA Scocchi M., Romeo D., Zanetti M.;  
RT "Molecular cloning of Bac7, a proline- and arginine-rich antimicrobial  
RT peptide from bovine neutrophils.";  
RL FEBS Lett. 352:197-200(1994).  
RN [2]







```
RP SEQUENCE FROM N.A.
RC STRAIN=HK10;
RX MEDLINE=21888633; PubMed=11891059; DOI=10.1016/S0378-1119(01)00899-X;
RA Shimizu T., Inoue T., Shiraishi H.;
RT "Cloning and characterization of novel extensin-like cDNAs that are
RT expressed during late somatic cell phase in the green alga Volvox
RT carteri.";
RL Gene 284:179-187(2002).
DR EMBL; AB070344; BAB85218.1; -.
DR InterPro; IPR008752; Peptidase M11.
DR InterPro; IPR006025; Pept M Zn_BS.
DR Pfam; PF05548; Peptidase M11; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 625 AA; 67803 MW; 050420F8A8A013BD CRC64;

Query Match 50.0%; Score 77.5; DB 2; Length 625;
Best Local Similarity 68.0%; Pred. No. 8.9;
Matches 17; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 2 RRPFPYLPRLPR-PRPPFFPPRLPPR 25
Db 586 RFPFPKPRPPRPP--PPRPPR 608

RESULT 10
TNF6_HUMAN STANDARD; PRT; 281 AA.
ID P48023; Q9BZP9;
AC 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (Apoptosis antigen ligand) (APL) (CD178 antigen).
GN Name=TNFSF6; Synonyms=APTLG1, FASL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
RT lymphocytes.";
RL J. Exp. Med. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
RT specificity.";
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX Schaeetzlein C.E., Poehlmann R., Philippssen P., Eibel H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioke T., Kasahara A.,
RA Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT "Isolation and characterization of a new naturally occurring variant of
RT human Fas ligand that is expressed only in membrane bound form.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
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RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
RX MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827;
RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
RA Tersikh A., Peitsch M.C., Tschopp J.;
RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
RL J. Biol. Chem. 272:18827-18833(1997).
RN [10]
RP PROCESSING.
RX MEDLINE=98087475; PubMed=9427603;
RA Tanaka M., Itai T., Adachi M., Nagata S.;
RT "Downregulation of Fas ligand by shedding.";
RL Nat. Med. 4:31-36(1998).
CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC modulates its effects.
CC -!- SUBUNIT: Homotrimer (Probable).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released
CC into the extracellular fluid, probably by cleavage from the cell
CC surface.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P48023-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
CC -!- PTM: N-glycosylated.
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing.
CC -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune
CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
CC involving hemolytic anemia and thrombocytopenia with massive
CC lymphadenopathy and splenomegaly.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674_g.htm".
CC -----
```





DE P0684B02.12 protein.  
GN Name=P0684B02.12;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12447438; DOI=10.1038/nature01184;  
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,  
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,  
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
RA Yano M., Jiang J., Gojobori T.;  
RT "The genome sequence and structure of rice chromosome 1.";  
RL Nature 420:312-316(2002).  
DR EMBL; AP003023; BAB44025.1; -.  
DR Gramene; Q94JF6; -.  
SQ SEQUENCE 185 AA; 20609 MW; 57FF2D5645DEC4A3 CRC64;

Query Match 49.4%; Score 76.5; DB 2; Length 185;  
Best Local Similarity 55.9%; Pred. No. 3.4;  
Matches 19; Conservative 0; Mismatches 6; Indels 9; Gaps 2;

QY 1 RRRPRPPYLP---RPRPPPPF-----PPRLPPR 25  
||||| ||| ||||| |||||  
Db 53 RRRPRDPLPALRRPDPPPAALRWDPRLHPR 86

RESULT 13  
Q94J98  
ID Q94J98 PRELIMINARY; PRT; 183 AA.  
AC Q94J98;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE P0047B08.14 protein (OJ1159 D09.5 protein).  
GN Name=P0047B08.14; Synonyms=OJ1159\_D09.5;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX PubMed=12447438; DOI=10.1038/nature01184;  
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,  
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,  
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,

RA Yano M., Jiang J., Gojobori T.;  
RT "The genome sequence and structure of rice chromosome 1.";  
RL Nature 420:312-316(2002).  
DR EMBL; AP003053; BAB55690.1; -.  
DR EMBL; AP003792; BAB89188.1; -.  
DR Gramene; Q94J98; -.  
SQ SEQUENCE 183 AA; 20155 MW; F1CF823AD89CEB36 CRC64;

Query Match 49.0%; Score 76; DB 2; Length 183;  
Best Local Similarity 51.5%; Pred. No. 3.7;  
Matches 17; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

QY 1 RRRPRPPYLP RPPPPPPFPP-----RLPP 24  
||||| ||| ||||| |||||  
Db 129 RSRPR-PYAPRPQPPQSPPLGRRRNAAVRRPP 160

RESULT 14  
Q9SBM1  
ID Q9SBM1 PRELIMINARY; PRT; 409 AA.  
AC Q9SBM1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hydroxyproline-rich glycoprotein DZ-HRGP precursor.  
GN Name=HRGP gene;  
OS Volvox carteri f. nagariensis.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Volvocaceae; Volvox.  
OX NCBI\_TaxID=3068;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HK10;  
RX MEDLINE=20044763; PubMed=10574980; DOI=10.1074/jbc.274.49.35023;  
RA Ender F., Hallmann A., Amon P., Sumper M.;  
RT "Response to the sexual pheromone and wounding in the green alga  
RT volvox: induction of an extracellular glycoprotein consisting almost  
RT exclusively of hydroxyproline.";  
RL J. Biol. Chem. 274:35023-35028(1999).  
DR EMBL; AJ242540; CAB62280.1; -.  
DR GO; GO:0005199; F:structural constituent of cell wall; IEA.  
DR InterPro; IPR003882; Pistil\_extensin.  
DR PRINTS; PR01218; PSTLEXTENSIN.  
KW Signal.  
FT SIGNAL 1 18 hydroxyproline-rich glycoprotein DZ-HRGP.  
FT CHAIN 18 409  
SQ SEQUENCE 409 AA; 41547 MW; CD0749C6AF02BD74 CRC64;

Query Match 49.0%; Score 76; DB 2; Length 409;  
Best Local Similarity 63.6%; Pred. No. 8.1;  
Matches 14; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 PRPPYLP RPPPPPPFPPRLPPR 25  
||||| ||| ||||| |||||  
Db 186 PRPPSPPPSPPPSPPPSPPPR 207

RESULT 15  
Q9YMX0  
ID Q9YMX0 PRELIMINARY; PRT; 1029 AA.  
AC Q9YMX0;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mucin-like protein.  
OS Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).  
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
OC Nucleopolyhedrovirus.  
OX NCBI\_TaxID=10449;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99124785; PubMed=9887315; DOI=10.1006/viro.1998.9469;  
RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,

Qy 1 RRRPPPYLRRRRPPPPFFPPRLPP 24  
925 RRRPPPYLRRRRPPPPFFPPRLPP 947

Search completed: October 26, 2005, 05:18:33  
Job time : 93.0546 secs



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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 26.7091 Seconds  
(without alignments)  
72.667 Million cell updates/sec

Title: US-10-014-147-2  
Perfect score: 155  
Sequence: 1 RRRPRPPYLPRRPPPPFFPRLPPRI 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	100.0	26	2	US-08-419-066-2
2	155	100.0	26	3	US-09-024-975-2
3	155	100.0	26	4	US-08-930-777A-2
4	155	100.0	38	4	US-09-739-535-1
5	155	100.0	39	1	US-08-162-052-1
6	155	100.0	39	1	US-08-310-722-1
7	155	100.0	39	2	US-08-419-066-1
8	155	100.0	39	2	US-08-728-333-1
9	155	100.0	39	3	US-09-024-975-1
10	155	100.0	39	4	US-08-930-777A-1
11	155	100.0	39	5	PCT-US95-12080-1
12	140	90.3	23	4	US-08-930-777A-3
13	116	74.8	19	4	US-08-930-777A-4
14	96	61.9	16	3	US-09-024-975-3
15	96	61.9	16	4	US-08-930-777A-5
16	83	53.5	14	3	US-09-024-975-4
17	83	53.5	14	4	US-08-930-777A-7
18	82	52.9	59	4	US-09-030-619-163
19	78	50.3	278	3	US-08-339-214-16
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22	78	50.3	278	4	US-09-246-129B-6
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29	77	49.7	281	3	US-09-479-524-3	Sequence 3, Appli
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31	77	49.7	281	3	US-08-339-214-30	Sequence 30, Appli
32	77	49.7	281	4	US-09-589-287B-6	Sequence 6, Appli
33	77	49.7	281	4	US-09-157-864-10	Sequence 10, Appl
34	77	49.7	281	4	US-09-006-755B-1	Sequence 1, Appli
35	77	49.7	281	4	US-09-027-287-6	Sequence 6, Appli
36	77	49.7	281	4	US-09-252-656B-6	Sequence 6, Appli
37	77	49.7	281	4	US-08-968-686-12	Sequence 12, Appl
38	77	49.7	281	4	US-09-588-947A-6	Sequence 6, Appli
39	77	49.7	281	4	US-09-589-286A-6	Sequence 6, Appli
40	77	49.7	281	4	US-09-523-323-6	Sequence 6, Appli
41	77	49.7	281	4	US-09-665-615B-25	Sequence 25, Appl
42	77	49.7	281	4	US-09-005-874-6	Sequence 6, Appli
43	77	49.7	281	4	US-09-255-794A-6	Sequence 6, Appli
44	77	49.7	281	4	US-09-507-968D-6	Sequence 6, Appli
45	77	49.7	281	5	PCT-US95-00362-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-419-066-2  
; Sequence 2, Application US/08419066  
; Patent No. 5830993  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &  
; ADDRESSEE: Collins  
; STREET: 2405 Grand Boulevard, Suite 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/419,066  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26262  
; REFERENCE/DOCKET NUMBER: 23625  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-08-419-066-2

Query Match 100.0%; Score 155; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 9e-10;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRPRPPYLPRRPPPPFFPRLPPRI 26



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; APPLICANT: MUTT, Viktor
; APPLICANT: JORNVAL, Hans
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,052
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 514
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9101838-2
; FILING DATE: 14-JUN-1991
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92-22578
; FILING DATE: 23-DEC-1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 003300-299
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-162-052-1
;
; Query Match 100.0%; Score 155; DB 1; Length 39;
; Best Local Similarity 100.0%; Pred. No. 1.3e-09;
; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RRRPPYLPRLPPPPFFPPRLPPRI 26
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Db 1 RRRPPYLPRLPPPPFFPPRLPPRI 26
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RESULT 6
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
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; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jorvall, Hans
; TITLE: No. 5654273el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
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US-08-310-722-1
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; Query Match 100.0%; Score 155; DB 1; Length 39;
; Best Local Similarity 100.0%; Pred. No. 1.3e-09;
; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 RRRPPYLPRLPPPPFFPPRLPPRI 26
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Db 1 RRRPPYLPRLPPPPFFPPRLPPRI 26
   |||||

RESULT 7
US-08-419-066-1
; Sequence 1, Application US/08419066
; Patent No. 5830993
;
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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STREET: 2405 Grand Blvd., Ste. 400  
CITY: Kansas City  
STATE: Missouri  
COUNTRY: U.S.A.  
ZIP: 64108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,777A  
FILING DATE: October 8, 1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/04674  
FILING DATE: April 10, 1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26,262  
REFERENCE/DOCKET NUMBER: 23625-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-930-777A-1

Query Match	100.0%	Score 155;	DB 4;	Length 39;
Best Local Similarity	100.0%;	Pred. NO. 1.3e-09;		
Matches 26:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 RRRPRPYLRPRPPPPPPPPRLPPI 26  
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db 1 RRRPRPYLRPRPPPPPPPPRLPPI 26  
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RESULT 11
PCT-US95-12080-1
; Sequence 1, Application PC/TUS9512080
; GENERAL INFORMATION:
; APPLICANT: Children's Medical Center Corporaton
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center.
; STREET: 1201 West Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12080
; FILING DATE:
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-815-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; PUBLICATION INFORMATION:  
 ; AUTHORS: Lee, Jong-Youn  
 ; AUTHORS: Boman, Hans G.  
 ; AUTHORS: Mutt, Viktor  
 ; AUTHORS: Jornvall, Hans  
 ; TITLE: Novel Polypeptides And Their Use  
 ; JOURNAL: PCT WO 92/22578  
 ; DATE: 12/23/92  
 ; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39  
 ; PCT-US95-12080-1

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Query Match      100.0%; Score 155; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. NO. 1.3e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	RRRRPPYL	RRRRPPRL	PPRI	26
QY					
db	1	RRRRPPYL <td>RRRRPPRL <td>PPRI <td>26</td> </td></td>	RRRRPPRL <td>PPRI <td>26</td> </td>	PPRI <td>26</td>	26

RESULT 12  
US-08-930-777A-3  
; Sequence 3, Application US/08930777A  
; Patent No. 6713605  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,777A  
FILING DATE: October 8, 1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/04674  
FILING DATE: April 10, 1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26,262  
REFERENCE/DOCKET NUMBER: 23625-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-930-777A-3

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Query Match          90.3%; Score 140; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
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OV 4 PRPPYLPRPPPPFFPPRLPPRI 26



Db 1 RPPYLPRLPPPPPPPPRLPPRI 23  
RESULT 13  
US-08-930-777A-4  
; Sequence 4, Application US/08930777A  
; Patent No. 6713605  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-930-777A-4  
Query Match 74.8%; Score 116; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.9e-06;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPPYLPRLPPPPPP 19  
Db 1 RRRPPYLPRLPPPPPP 19  
RESULT 14  
US-09-024-975-3  
; Sequence 3, Application US/09024975  
; Patent No. 6133233  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, CHRISTOPHER R.  
; APPLICANT: BLECHA, FRANK  
; APPLICANT: SHI, JISHU  
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
; STREET: 2405 GRAND BLVD., SUITE 400  
; CITY: KANSAS CITY  
; STATE: MO  
; COUNTRY: USA

; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/024,975  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/802,306  
; FILING DATE: 18-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COLLINS, JOHN M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 25585-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 816/474-9050  
; TELEFAX: 816/474-9057  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-024-975-3  
Query Match 61.9%; Score 96; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00052;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 RRRPPPPPPRLPPRI 26  
Db 1 RRRPPPPPPRLPPRI 16  
RESULT 15  
US-08-930-777A-5  
; Sequence 5, Application US/08930777A  
; Patent No. 6713605  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057

;  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-930-777A-5

Query Match 61.9%; Score 96; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00052;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RPRPPPPPPRLPPRI 16

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:05:05 ; Search time 95.9636 Seconds  
(without alignments)  
113.119 Million cell updates/sec

Title: US-10-014-147-2

Perfect score: 155

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	100.0	26	14 US-10-014-147-2	Sequence 2, Appli
2	155	100.0	26	15 US-10-014-147-2	Sequence 2, Appli
3	155	100.0	38	9 US-09-738-742-1	Sequence 1, Appli
4	155	100.0	38	9 US-09-739-535-1	Sequence 1, Appli
5	155	100.0	39	14 US-10-014-147-1	Sequence 1, Appli
6	155	100.0	39	15 US-10-391-155-1	Sequence 1, Appli
7	155	100.0	39	15 US-10-391-155-2	Sequence 2, Appli
8	155	100.0	39	15 US-10-391-155-6	Sequence 6, Appli
9	155	100.0	39	15 US-10-014-147-1	Sequence 1, Appli
10	155	100.0	42	16 US-10-344-709C-18	Sequence 18, Appli
11	155	100.0	42	17 US-10-916-185-14	Sequence 14, Appli

12	155	100.0	42	18 US-10-991-286A-44	Sequence 44, Appli
13	155	100.0	42	20 US-11-004-379-20	Sequence 20, Appli
14	140	90.3	23	14 US-10-014-147-3	Sequence 3, Appli
15	140	90.3	23	15 US-10-651-147-3	Sequence 3, Appli
16	116	74.8	19	14 US-10-014-147-4	Sequence 4, Appli
17	116	74.8	19	15 US-10-651-147-4	Sequence 4, Appli
18	96	61.9	16	14 US-10-014-147-5	Sequence 5, Appli
19	96	61.9	16	15 US-10-651-147-5	Sequence 5, Appli
20	91	58.7	91	16 US-10-425-115-200180	Sequence 200180,
21	90	58.1	15	15 US-10-391-155-3	Sequence 3, Appli
22	89.5	57.7	304	14 US-10-156-761-13550	Sequence 13550, A
23	86.5	55.8	200	16 US-10-425-115-206766	Sequence 206766,
24	84.5	54.5	322	16 US-10-425-115-316075	Sequence 316075,
25	84	54.2	182	16 US-10-425-115-232475	Sequence 232475,
26	83.5	53.9	245	16 US-10-425-115-206869	Sequence 206869,
27	83	53.5	14	14 US-10-014-147-7	Sequence 7, Appli
28	83	53.5	14	15 US-10-651-147-7	Sequence 7, Appli
29	83	53.5	86	16 US-10-437-963-131741	Sequence 131741,
30	83	53.5	192	16 US-10-437-963-143333	Sequence 143333,
31	82.5	53.2	276	16 US-10-437-963-132896	Sequence 132896,
32	82	52.9	59	9 US-09-030-619-163	Sequence 163, App
33	82	52.9	59	9 US-09-912-609-51	Sequence 51, Appli
34	82	52.9	59	15 US-10-277-232-163	Sequence 163, App
35	82	52.9	59	15 US-10-277-233-163	Sequence 163, App
36	82	52.9	59	17 US-10-838-289-683	Sequence 683, App
37	82	52.9	60	16 US-10-344-709C-17	Sequence 17, Appli
38	81.5	52.6	80	15 US-10-424-599-231660	Sequence 231660,
39	81.5	52.6	483	16 US-10-437-963-191498	Sequence 191498,
40	81	52.3	163	16 US-10-437-963-144892	Sequence 144892,
41	81	52.3	179	16 US-10-767-701-35404	Sequence 35404, A
42	80.5	51.9	255	16 US-10-425-115-316074	Sequence 316074,
43	80.5	51.9	284	16 US-10-425-115-316071	Sequence 316071,
44	80	51.6	109	15 US-10-424-599-267648	Sequence 267648,
45	80	51.6	132	16 US-10-767-701-51171	Sequence 51171, A

ALIGNMENTS

RESULT 1  
US-10-014-147-2  
; Sequence 2, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/014,147  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-014-147-2
Query Match 100.0%; Score 155; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26
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Db 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26

RESULT 2
US-10-651-147-2
; Sequence 2, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/651,147
; FILING DATE: 28-Aug-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-651-147-2
Query Match 100.0%; Score 155; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26
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Db 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26

RESULT 3
US-09-738-742-1
; Sequence 1, Application US/09738742
; Publication No. US20020025924A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/738,742
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-738-742-1
Query Match 100.0%; Score 155; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26
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Db 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26

RESULT 4
US-09-739-535-1
; Sequence 1, Application US/09739535
; Publication No. US20020058785A1
; GENERAL INFORMATION:
; APPLICANT: Cubist Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS
; FILE REFERENCE: C060
; CURRENT APPLICATION NUMBER: US/09/739,535
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-739-535-1
Query Match 100.0%; Score 155; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 RRRPRPPYLPRPRPPPPFFPPRLPPRI 26

RESULT 5
US-10-014-147-1
; Sequence 1, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
;
```







```

; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: MODIFIED iRNA AGENTS
; FILE REFERENCE: 14174-091001
; CURRENT APPLICATION NUMBER: US/10/916,185
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 60/510,246
; PRIOR FILING DATE: 2003-10-09
; Remaining Prior Application data removed -
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSEO for Windows Version 4.0

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Query Match      100.0%; Score 155; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RRRRPPYLPRRPPPPPPPPRLLPPRI 26

pB 1 RRRRPPYLPRRPPPPPPPPRLLPPRI 26

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RESULT 12
US-10-991-286A-44
; Sequence 44, Application US/10991286A
; Publication No. US20050186591A1
; GENERAL INFORMATION:
; APPLICANT: Bumcrot, David
; APPLICANT: Farrer, Matthew J.
; APPLICANT: Maraganore, Demetrius M.
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: METHOD OF TREATING NEURODEGENERATIVE DISEASE
; FILE REFERENCE: 17574-003001
; CURRENT APPLICATION NUMBER: US/10/991,286A
; CURRENT FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: PCT/US2004/18271
; PRIOR FILING DATE: 2004-06-09
; PRIOR APPLICATION NUMBER: US 60/476,947
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptide
US-10-991-286A-44

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Query Match 100.0%; Score 155; DB 18; Length 42;

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Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY					
Db	1	RRRRPPYLP <td>RRRRPPPPPPPP <td>RRPPRI <td>26</td> </td></td>	RRRRPPPPPPPP <td>RRPPRI <td>26</td> </td>	RRPPRI <td>26</td>	26

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RESULT 13
US-11-004-379-20
; Sequence 20, Application US/11004379
; Publication NO. US2005015337A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: iRNA CONJUGATES
; FILE REFERENCE: 14174-067001
; CURRENT APPLICATION NUMBER: US/11/004,379
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/US04/10586
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/460,783
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/462,894
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permea
US-11-004-379-20

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Query Match	100.0%;	Score 155;	DB 20;	Length 42;
Best Local Similarity	100.0%;	Pred. No. 1.2e-07;		
Matches 26:	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy	1	RRRRPPYL	RRRRPPPPPPPPPPPPRL	PPRI	26
Qy					
ph	1	RRRRPPYL <td>RRRRPPPPPPPPPPPPRL <td>PPRI</td> <td>26</td> </td>	RRRRPPPPPPPPPPPPRL <td>PPRI</td> <td>26</td>	PPRI	26

RESULT 14  
US-10-014-147-3  
; Sequence 3, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.

ZIP: 64108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/014,147  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,777A  
FILING DATE: October 8, 1997  
APPLICATION NUMBER: PCT/US96/04674  
FILING DATE: April 10, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26,262  
REFERENCE/DOCKET NUMBER: 23625-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-014-147-3

Query Match 90.3%; Score 140; DB 14; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PRPPYLPRPRPPPPFPPRLPPRI 26  
Db 1 PRPPYLPRPRPPPPFPPRLPPRI 23

RESULT 15  
US-10-651-147-3  
Sequence 3, Application US/10651147  
Publication No. US20040043934A1  
GENERAL INFORMATION:  
APPLICANT: Blecha, Frank  
Shi, Jishu  
TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hovey, Williams, Timmons & Collins  
STREET: 2405 Grand Blvd., Ste. 400  
CITY: Kansas City  
STATE: Missouri  
COUNTRY: U.S.A.  
ZIP: 64108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/651,147  
FILING DATE: 28-Aug-2003  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,777A  
FILING DATE: October 8, 1997  
APPLICATION NUMBER: PCT/US96/04674  
FILING DATE: April 10, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26,262

REFERENCE/DOCKET NUMBER: 23625-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-651-147-3  
Query Match 90.3%; Score 140; DB 15; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PRPPYLPRPRPPPPFPPRLPPRI 26  
Db 1 PRPPYLPRPRPPPPFPPRLPPRI 23  
Search completed: October 26, 2005, 05:28:56  
Job time : 96.9636 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 04:51:43 ; Search time 62.9818 Seconds  
(without alignments)  
98.253 Million cell updates/sec

Title: US-10-014-147-5  
Perfect score: 96  
Sequence: 1 RPRPPPPFFPPLPPRI 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB ID	Description
	Score	Match				
1	96	100.0	16	2	AAW01448	Aaw01448 Leukocyte
2	96	100.0	16	2	AAW75724	Aaw75724 Proline/A
3	96	100.0	16	8	ADE86116	Ade86116 Proline-a
4	96	100.0	16	8	ADL67258	Adl67258 Antimicro
5	96	100.0	23	2	AAW01451	Aaw01451 Leukocyte
6	96	100.0	23	8	ADE86114	Ade86114 Proline-a
7	96	100.0	23	8	ADL67256	Adl67256 Antimicro
8	96	100.0	26	2	AAW01447	Aaw01447 Leukocyte
9	96	100.0	26	2	AAW75723	Aaw75723 Proline/A
10	96	100.0	26	8	ADE86113	Ade86113 Proline-a
11	96	100.0	26	8	ADL67255	Adl67255 Antimicro
12	96	100.0	39	2	AAR30491	Aar30491 Antibacte
13	96	100.0	39	2	AAR99121	Aar99121 Magainin-
14	96	100.0	39	2	AAR94446	Aar94446 Synducin
15	96	100.0	39	2	AAW01446	Aaw01446 Leukocyte
16	96	100.0	39	2	AAW75722	Aaw75722 Proline/A
17	96	100.0	39	3	AAB26888	Aab26888 PR-39 pep
18	96	100.0	39	4	AAB97280	Aab97280 PR-39 pep
19	96	100.0	39	4	AAB84690	Aab84690 Amino aci
20	96	100.0	39	8	ADD35364	Add35364 Antimicro
21	96	100.0	39	8	ADE86112	Ade86112 Proline-a
22	96	100.0	39	8	ADL67254	Adl67254 Antimicro
23	96	100.0	42	5	ABB07714	Abb07714 Antimicro
24	96	100.0	42	8	ADR82250	Adr82250 Cell perm
25	96	100.0	44	4	AAB51194	Aab51194 E. coli A

26	63	65.6	311	2	AAW17387	Aay17387 Human DNA
27	60	62.5	520	4	ABU52849	Abu52849 Human ute
28	60	62.5	521	2	AAW74802	Aaw74802 Human sec
29	60	62.5	521	5	ABG95252	Abg95252 Human nov
30	60	62.5	521	6	ABO34446	Abo34446 Region of
31	60	62.5	521	7	ADI23107	Adi23107 Novel hum
32	60	62.5	521	8	ADH74109	Adh74109 Human sec
33	60	62.5	526	3	AAB56895	Aab56895 Human pro
34	60	62.5	535	7	ADC31125	Adc31125 Human nov
35	60	62.5	565	4	AAM78694	Aam78694 Human pro
36	60	62.5	594	4	AAW72162	Aay72162 Human RNA
37	60	62.5	594	8	ADQ96576	Adq96576 T cell ac
38	59	61.5	599	4	AAU15847	Aau15847 Human nov
39	59	61.5	209	6	ABU54916	Abu54916 Human nov
40	59	61.5	292	4	AAU16308	Aau16308 Human nov
41	59	61.5	292	6	ABU55377	Abu55377 Human nov
42	59	61.5	313	2	AAW02613	Aay02613 Protein e
43	59	61.5	347	4	ABB50177	Abb50177 Human tra
44	59	61.5	347	7	ADB64690	Adb64690 Human pro
45	59	61.5	347	7	ADC31185	Adc31185 Human nov

ALIGNMENTS

RESULT 1  
AAW01448  
ID AAW01448 standard; peptide; 16 AA.

XX AC AAW01448;

XX DT 18-JUN-1997 (first entry)

XX DE Leukocyte O2- production inhibitor peptide PR16.

XX KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;  
antimicrobial peptide; small intestine; human; neutrophil; bacteria;  
DNA synthesis; protein synthesis; inhibitor; syndecan expression;  
mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;  
tissue damage; oxygen radical; inflammatory disease; therapy.

XX OS Synthetic.

XX PN WO9632129-A1.

XX PD 17-OCT-1996.

XX PF 10-APR-1996; 96WO-US004674.

XX PR 10-APR-1995; 95US-00419066.

XX PA (UNIV ) UNIV KANSAS STATE RES FOUND.

XX PI Blecha F, Shi J;

XX DR WPI; 1996-476842/47.

XX PT Inhibition of leukocyte super:oxide anion prodn. and attraction of  
leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX PS Claim 12; Page 28; 45pp; English.

XX CC AAW01447-W01454 represent fragments of the proline-arginine rich  
antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first  
isolated from porcine small intestine, and has also been identified in  
human and porcine neutrophils. PR39 kills bacteria by interfering with  
DNA and/or protein synthesis. PR39 also induces syndecan expression on  
mesenchymal cells. Syndecans are important in wound repair, showing that  
PR39 can be used in wound repair, as well as in antibacterial agents.  
These sequences, and PR39, can be used in the method of the invention.  
The method of the invention is for inhibiting leukocyte superoxide anion  
(O2-) production. The method comprises administering to a leukocyte a  
peptide (such as this sequence) capable of inhibiting leukocyte O2-



CC production. The peptides can be used as medicaments for fighting  
CC infection by attracting leukocytes to a wound site and restricting tissue  
CC damage at the wound site caused by excessive oxygen radicals produced by  
CC these leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states  
XX  
SQ Sequence 16 AA;

Query Match 100.0%; Score 96; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPRPPPPFPRLPPRI 16  
| | | | | | | | | | | | | | | |  
Db 1 RPRPPPPFPRLPPRI 16

RESULT 2  
AAW75724  
ID AAW75724 standard; peptide; 16 AA.  
XX  
AC AAW75724;  
XX  
DT 19-NOV-1998 (first entry)  
XX  
DE Proline/Arginine rich peptide.  
XX  
KW Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;  
KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;  
KW coronary bypass; organ transplantation surgery.  
XX  
OS Synthetic.  
XX  
PN WO9835690-A1.  
XX  
PD 20-AUG-1998.  
XX  
PF 17-FEB-1998; 98WO-US003207.  
XX  
PR 18-FEB-1997; 97US-00802306.  
PR 16-FEB-1998; 98US-00024975.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
PI Ross CR, Blecha F, Shi J;  
XX  
DR WPI; 1998-495359/42.  
XX  
PT Reduction of reperfusion injury in temporarily occluded blood vessels -  
PT by administration of a peptide which is rich in proline or arginine  
PT residues.  
XX  
PS Claim 3; Page 15; 35pp; English.  
XX

Sequences AAW75722-W75732 are proline/arginine rich peptides that upon  
administration into a mammal's bloodstream reduce reperfusion injury  
(production of reactive oxygen species, neutrophil adherence to  
endothelium, and extravasation of neutrophils). These peptides have two  
requirements: they contain the consensus sequence PXXP, where P is a  
proline residue and X is any amino acid residue, which has been found to  
inhibit superoxide production, and secondly they have arginine residues  
adjacent to these motifs, required for effective inhibition. It was  
established by structural and function analysis that a peptide should  
ideally contain 4 or 6 of these motifs, and that inhibitory activity is  
correlated with the increase of length of peptides. The effectiveness of  
these peptides was determined by investigating the production of the  
neutrophil superoxide anion, and also the inhibition of neutrophil  
chemotaxis. From this, it was found that all of the peptides inhibited  
NADPH oxidase to some extent. All of the peptides also inhibit neutrophil  
oxidase activity. PR-39 is believed, to be the most potent endogenous  
down regulator of NADPH oxidase yet discovered, and from the data  
produced, it can be suggested to be involved in eliminating or reducing  
the reperfusion injury induced adhesion and extraction of neutrophils.

CC The peptides are also useful in connection with surgical procedures such  
CC as coronary bypass and organ transplantation surgery  
XX  
SQ Sequence 16 AA;

Query Match 100.0%; Score 96; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPRPPPPFPRLPPRI 16  
| | | | | | | | | | | | | | | |  
Db 1 RPRPPPPFPRLPPRI 16

RESULT 3  
ADE86116  
ID ADE86116 standard; peptide; 16 AA.  
XX  
AC ADE86116;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Proline-arginine (PR)-rich antimicrobial peptide PR-16.  
XX  
KW Leukocyte superoxide anion; leukocyte O2- production;  
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;  
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;  
KW tissue damage; oxygen radical; antibacterial.  
XX  
OS Synthetic.  
XX  
PN US2003125249-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 07-DEC-2001; 2001US-00014147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 2004-059188/06.  
XX  
PT Attracting leukocyte to location by administering peptide including  
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to  
PT the location.  
XX  
PS Claim 3; SEQ ID NO 5; 24pp; English.  
XX

The present invention relates to a method of inhibiting leukocyte  
superoxide anion (O2-) production and/or attracting leukocytes. The  
method comprises the use of proline-arginine (PR)-rich antimicrobial  
peptides or their truncated analogues. The method is useful for  
attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or  
a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are  
useful as medicaments to fight infection by attracting leukocytes to a  
wound site, while restricting tissue damage at the wound site caused by  
excessive oxygen radicals produced by these leukocytes. The present  
sequence represents a PR-rich antimicrobial peptide.

Query Match 100.0%; Score 96; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPRPPPPFPRLPPRI 16  
| | | | | | | | | | | | | | | |  
Db 1 RPRPPPPFPRLPPRI 16

RESULT 4  
ADL67258  
ID ADL67258 standard; peptide; 16 AA.  
XX  
AC ADL67258;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39 analog PR-16.  
XX  
KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;  
KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;  
KW infection; wound; tissue damage; PR-39 analog; PR-16.  
XX  
OS Unidentified.  
XX  
PN US2004043934-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 28-AUG-2003; 2003US-00651147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 2004-225728/21.  
XX  
PT Inhibiting leukocyte oxygen radical production comprises contacting a  
PT leukocyte with a peptide, where the inhibition occurs as a consequence of  
PT binding between the peptide and p47phox.  
XX  
PS Claim 9; SEQ ID NO 5; 24pp; English.  
XX  
CC The invention relates to inhibiting leukocyte superoxide anion (O2-)  
CC production using a naturally occurring proline-arginine (PR)-rich  
CC antimicrobial peptide known as PR-39 and its truncated analogs. The  
CC method comprises contacting leukocytes with the peptide comprising 39 or  
CC 26 amino acids, for a time and under conditions effective to inhibit  
CC leukocyte superoxide anion production. The peptide inhibits the activity  
CC of NADPH oxidase responsible for anion production, by binding to Src  
CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein  
CC of the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or  
CC porcine leucocyte and the mammalian leucocyte is neutrophil. Another  
CC method is also disclosed which employs a PR-39 analog that comprise 16  
CC amino acids, where the sum of the proline and arginine residues in the  
CC effective peptide is at least 66 or 74 % of the total number of amino  
CC acids. This peptide inhibits leucocyte O2- production by the effective  
CC binding to p47phox in whole cells, therefore interfering with the binding  
CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in  
CC the peptide are arginine residues. The method of the invention is useful  
CC for inhibiting leucocyte oxygen radical production. The peptides are  
CC useful as medicaments for fighting infections by attracting leucocytes to  
CC a wound site, yet restrict tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leucocytes. The present  
CC sequence is PR-39 analog, PR-16.  
XX  
SQ Sequence 16 AA;

Query Match 100.0%; Score 96; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RPRPPPPFPRLPPRI 16  
| | | | | | | | | | | | | | | |  
Db 1 RPRPPPPFPRLPPRI 16

RESULT 5  
AAW01451  
ID AAW01451 standard; peptide; 23 AA.  
XX  
AC AAW01451;  
XX  
DT 18-JUN-1997 (first entry)  
XX  
DE Leucocyte O2- production inhibitor peptide PR23.  
XX  
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;  
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;  
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;  
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;  
KW tissue damage; oxygen radical; inflammatory disease; therapy.  
XX  
OS Synthetic.  
XX  
PN WO9632129-A1.  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-US004674.  
XX  
PR 10-APR-1995; 95US-00419066.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 1996-476842/47.  
XX  
PT Inhibition of leukocyte super:oxide anion prodn. and attraction of  
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.  
XX  
PS Disclosure; Page 27; 45pp; English.  
XX  
CC AAW01447-W01454 represent fragments of the proline-arginine rich  
CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first  
CC isolated from porcine small intestine, and has also been identified in  
CC human and porcine neutrophils. PR39 kills bacteria by interfering with  
CC DNA and/or protein synthesis. PR39 also induces syndecan expression on  
CC mesenchymal cells. Syndecans are important in wound repair, showing that  
CC PR39 can be used in wound repair, as well as in antibacterial agents.  
CC These sequences, and PR39, can be used in the method of the invention.  
CC The method of the invention is for inhibiting leukocyte superoxide anion  
CC (O2-) production. The method comprises administering to a leukocyte a  
CC peptide (such as this sequence) capable of inhibiting leukocyte O2-  
CC production. The peptides can be used as medicaments for fighting  
CC infection by attracting leukocytes to a wound site and restricting tissue  
CC damage at the wound site caused by excessive oxygen radicals produced by  
CC these leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states  
XX  
SQ Sequence 23 AA;

Query Match 100.0%; Score 96; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.00023;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RPRPPPPFPRLPPRI 16  
| | | | | | | | | | | | | | | |  
Db 8 RPRPPPPFPRLPPRI 23

RESULT 6  
ADE86114  
ID ADE86114 standard; peptide; 23 AA.  
XX  
AC ADE86114;  
XX  
DT 29-JAN-2004 (first entry)

XX	Proline-arginine (PR)-rich antimicrobial peptide PR-23.	XX	28-AUG-2003; 2003US-006511147.
DE		PF	
XX		XX	
KW	Leukocyte superoxide anion; leukocyte O2- production;	PR	10-APR-1995; 95US-00419066.
KW	leukocyte attraction; proline-arginine-rich antimicrobial peptide;	PR	08-OCT-1997; 97US-00930777.
KW	PR-rich antimicrobial peptide; neutrophil; wound site; infection;	XX	
KW	tissue damage; oxygen radical; antibacterial.	PA	(BLEC/) BLECHA F.
XX		PA	(SHIJ/) SHI J.
OS	Synthetic.	XX	
XX		PI	Blecha F, Shi J;
PN	US2003125249-A1.	XX	
XX	03-JUL-2003.	XX	
PD		DR	WPI; 2004-225728/21.
XX		XX	
XX	07-DEC-2001; 2001US-00014147.	PT	Inhibiting leukocyte oxygen radical production comprises contacting a
PF		PT	leukocyte with a peptide, where the inhibition occurs as a consequence of
XX		PT	binding between the peptide and p47phox.
PR	10-APR-1995; 95US-00419066.	XX	
PR	08-OCT-1997; 97US-00930777.	PS	Example; SEQ ID NO 3; 24pp; English.
XX		XX	
PA	(BLEC/) BLECHA F.	CC	The invention relates to inhibiting leukocyte superoxide anion (O2-) production using a naturally occurring proline-arginine (PR)-rich
PA	(SHIJ/) SHI J.	CC	antimicrobial peptide known as PR-39 and its truncated analogs. The
XX		CC	method comprises contacting leukocytes with the peptide comprising 39 or
PI	Blecha F, Shi J;	CC	26 amino acids, for a time and under conditions effective to inhibit
XX		CC	leucocyte superoxide anion production. The peptide inhibits the activity
XX	WPI; 2004-059188/06.	CC	of NADPH oxidase responsible for anion production, by binding to Src
DR		CC	homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein
XX	Attracting leukocyte to location by administering peptide including	CC	of the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or
PT	proline-arginine-rich antimicrobial peptide or its truncated analogs to	CC	porcine leucocyte and the mammalian leucocyte is neutrophil. Another
PT	the location.	CC	method is also disclosed which employs a PR-39 analog that comprise 16
XX		CC	amino acids, where the sum of the proline and arginine residues in the
PS	Example; SEQ ID NO 3; 24pp; English.	CC	effective peptide is at least 66 or 74 % of the total number of amino
XX		CC	acids. This peptide inhibits leucocyte O2- production by the effective
CC	The present invention relates to a method of inhibiting leukocyte	CC	binding to p47phox in whole cells, therefore interfering with the binding
CC	superoxide anion (O2-) production and/or attracting leukocytes. The	CC	of p47phox to p22phox. At least 14 or 25% of the amino acid residues in
CC	method comprises the use of proline-arginine (PR)-rich antimicrobial	CC	the peptide are arginine residues. The method of the invention is useful
CC	peptides or their truncated analogues. The method is useful for	CC	for inhibiting leukocyte oxygen radical production. The peptides are
CC	attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or	CC	useful as medicaments for fighting infections by attracting leucocytes to
CC	a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are	CC	a wound site, yet restrict tissue damage at the wound site caused by
CC	useful as medicaments to fight infection by attracting leukocytes to a	CC	excessive oxygen radicals produced by these leucocytes. The present
CC	wound site, while restricting tissue damage at the wound site caused by	CC	sequence is PR-39 analog, PR-23.
CC	excessive oxygen radicals produced by these leukocytes. The present	XX	
CC	sequence represents a PR-rich antimicrobial peptide.	SQ	Sequence 23 AA;
XX			
SQ	Sequence 23 AA;		
	Query Match 100.0%; Score 96; DB 8; Length 23;		Query Match 100.0%; Score 96; DB 8; Length 23;
	Best Local Similarity 100.0%; Pred. No. 0.00023;		Best Local Similarity 100.0%; Pred. No. 0.00023;
	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RPRPPPPFPRLPPRI 16	QY	1 RPRPPPPFPRLPPRI 16
	f		f
Db	8 RPRPPPPFPRLPPRI 23	Db	8 RPRPPPPFPRLPPRI 23
RESULT 7		RESULT 8	
ADL67256		AAW01447	
ID	ADL67256 standard; peptide; 23 AA.	ID	AAW01447 standard; peptide; 26 AA.
XX		XX	
AC	ADL67256;	AC	AAW01447;
XX		XX	
DT	20-MAY-2004 (first entry)	DT	18-JUN-1997 (first entry)
XX		XX	
DE	Antimicrobial peptide PR-39 analog PR-23.	DE	Leukocyte O2- production inhibitor peptide PR26.
KW	Leucocyte; superoxide anion; oxygen radical; proline-arginine;	KW	Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
KW	antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;	KW	antimicrobial peptide; small intestine; human; neutrophil; bacteria;
KW	infection; wound; tissue damage; PR-39 analog; PR-23.	KW	DNA synthesis; protein synthesis; inhibitor; syndecan expression;
XX		KW	mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
OS	Unidentified.	KW	tissue damage; oxygen radical; inflammatory disease; therapy.
XX		XX	
PN	US2004043934-A1.	OS	Synthetic.
XX		XX	
PD	04-MAR-2004.	PN	WO9632129-A1.
		XX	

PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-US004674.  
XX  
PR 10-APR-1995; 95US-00419066.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;

XX WPI; 1996-476842/47.

XX Inhibition of leukocyte super:oxide anion prodn. and attraction of  
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX Claim 3; Page 26; 45pp; English.

XX AAW01447-W01454 represent fragments of the proline-arginine rich  
CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first  
CC isolated from porcine small intestine, and has also been identified in  
CC human and porcine neutrophils. PR39 kills bacteria by interfering with  
CC DNA and/or protein synthesis. PR39 also induces syndecan expression on  
CC mesenchymal cells. Syndecans are important in wound repair, showing that  
CC PR39 can be used in wound repair, as well as in antibacterial agents.  
CC These sequences, and PR39, can be used in the method of the invention.  
CC The method of the invention is for inhibiting leukocyte superoxide anion  
CC (O2-) production. The method comprises administering to a leukocyte a  
CC peptide (such as this sequence) capable of inhibiting leukocyte O2-  
CC production. The peptides can be used as medicaments for fighting  
CC infection by attracting leukocytes to a wound site and restricting tissue  
CC damage at the wound site caused by excessive oxygen radicals produced by  
CC these leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states

XX Sequence 26 AA;

Query Match 100.0%; Score 96; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 9  
AAW75723

ID AAW75723 standard; peptide; 26 AA.

XX AAW75723;

XX 19-NOV-1998 (first entry)

XX Proline/Arginine rich peptide PR-26.

XX Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;  
KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;  
KW coronary bypass; organ transplantation surgery.

XX Synthetic.

XX WO9835690-A1.

XX 20-AUG-1998.

XX 17-FEB-1998; 98WO-US003207.

XX 18-FEB-1997; 97US-00802306.

XX 16-FEB-1998; 98US-00024975.

XX (UNIV ) UNIV KANSAS STATE RES FOUND.

XX Ross CR, Blecha F, Shi J;

XX WPI; 1998-495359/42.

XX Reduction of reperfusion injury in temporarily occluded blood vessels -  
PT by administration of a peptide which is rich in proline or arginine  
PT residues.

XX Claim 3; Page 14-15; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon  
CC administration into a mammal's bloodstream reduce reperfusion injury  
CC (production of reactive oxygen species, neutrophil adherence to  
CC endothelium, and extravasation of neutrophils). These peptides have two  
CC requirements: they contain the consensus sequence PXXP, where P is a  
CC proline residue and X is any amino acid residue, which has been found to  
CC inhibit superoxide production, and secondly they have arginine residues  
CC adjacent to these motifs, required for effective inhibition. It was  
CC established by structural and function analysis that a peptide should  
CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is  
CC correlated with the increase of length of peptides. The effectiveness of  
CC these peptides was determined by investigating the production of the  
CC neutrophil superoxide anion, and also the inhibition of neutrophil  
CC chemotaxis. From this, it was found that all of the peptides inhibited  
CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil  
CC oxidase activity. PR-39 is believed, to be the most potent endogenous  
CC down regulator of NADPH oxidase yet discovered, and from the data  
CC produced, it can be suggested to be involved in eliminating or reducing  
CC the reperfusion injury induced adhesion and extraction of neutrophils.  
CC The peptides are also useful in connection with surgical procedures such  
CC as coronary bypass and organ transplantation surgery

XX Sequence 26 AA;

Query Match 100.0%; Score 96; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 10  
ADE86113

ID ADE86113 standard; peptide; 26 AA.

XX ADE86113;

XX 29-JAN-2004 (first entry)

XX Proline-arginine (PR)-rich antimicrobial peptide PR-26.

XX Leukocyte superoxide anion; leukocyte O2- production;  
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;  
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;  
KW tissue damage; oxygen radical; antibacterial.

XX Synthetic.

XX US2003125249-A1.

XX 03-JUL-2003.

XX 07-DEC-2001; 2001US-00014147.

XX 10-APR-1995; 95US-00419066.

XX 08-OCT-1997; 97US-00930777.

XX (BLEC/) BLECHA F.

XX (SHIJ/) SHI J.

XX Blecha F, Shi J;

XX



DR WPI; 2004-059188/06.  
XX  
PT Attracting leukocyte to location by administering peptide including  
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to  
PT the location.  
XX  
PS Claim 3; SEQ ID NO 2; 24pp; English.  
XX  
CC The present invention relates to a method of inhibiting leukocyte  
CC superoxide anion (O2-) production and/or attracting leukocytes. The  
CC method comprises the use of proline-arginine (PR)-rich antimicrobial  
CC peptides or their truncated analogues. The method is useful for  
CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or  
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are  
CC useful as medicaments to fight infection by attracting leukocytes to a  
CC wound site, while restricting tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leukocytes. The present  
CC sequence represents a PR-rich antimicrobial peptide.  
XX  
SQ Sequence 26 AA;  
  
Query Match 100.0%; Score 96; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RPRPPPPFPRLPPRI 16  
Db 11 RPRPPPPFPRLPPRI 26  
  
RESULT 11  
ADL67255  
ID ADL67255 standard; peptide; 26 AA.  
XX  
AC ADL67255;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39 analog PR-26.  
XX  
KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;  
KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;  
KW infection; wound; tissue damage; PR-39 analog; PR-26.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Region 1. .3  
FT /note= "Essential for antibacterial activity"  
FT Region 20. .26  
FT /note= "Essential for antibacterial activity"  
XX  
PN US2004043934-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 28-AUG-2003; 2003US-00651147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 2004-225728/21.  
XX  
PT Inhibiting leukocyte oxygen radical production comprises contacting a  
PT leukocyte with a peptide, where the inhibition occurs as a consequence of  
PT binding between the peptide and p47phox.  
XX  
PS Claim 1; SEQ ID NO 2; 24pp; English.

XX The invention relates to inhibiting leukocyte superoxide anion (O2-) production using a naturally occurring proline-arginine (PR)-rich antimicrobial peptide known as PR-39 and its truncated analogs. The method comprises contacting leukocytes with the peptide comprising 39 or 26 amino acids, for a time and under conditions effective to inhibit leukocyte superoxide anion production. The peptide inhibits the activity of NADPH oxidase responsible for anion production, by binding to Src homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or porcine leukocyte and the mammalian leukocyte is neutrophil. Another method is also disclosed which employs a PR-39 analog that comprise 16 amino acids, where the sum of the proline and arginine residues in the effective peptide is at least 66 or 74 % of the total number of amino acids. This peptide inhibits leukocyte O2- production by the effective binding to p47phox in whole cells, therefore interfering with the binding of p47phox to p22phox. At least 14 or 25% of the amino acid residues in the peptide are arginine residues. The method of the invention is useful for inhibiting leukocyte oxygen radical production. The peptides are useful as medicaments for fighting infections by attracting leukocytes to a wound site, yet restrict tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence is PR-39 analog PR-26.  
XX  
SQ Sequence 26 AA;  
  
Query Match 100.0%; Score 96; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RPRPPPPFPRLPPRI 16  
Db 11 RPRPPPPFPRLPPRI 26  
  
RESULT 12  
AAR30491  
ID AAR30491 standard; peptide; 39 AA.  
XX  
AC AAR30491;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-MAY-1993 (first entry)  
XX  
DE Antibacterial peptide.  
XX  
KW Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;  
KW veterinary medicine; prophylactic.  
XX  
OS Sus scrofa domestica.  
XX  
PN WO9222578-A1.  
XX  
PD 23-DEC-1992.  
XX  
PF 10-JUN-1992; 92WO-SE000394.  
XX  
PR 14-JUN-1991; 91SE-00001838.  
XX  
PA (LEEJ/) LEE J.  
PA (BOMA/) BOMAN H G.  
PA (MUTT/) MUTT V.  
PA (JOER/) JOERNVALL H.  
XX  
PI Lee J, Boman HG, Mutt V, Joernvall H;  
XX  
DR WPI; 1993-018080/02.  
XX  
PT New anti-bacterial polypeptide - active against Gram negative bacteria.  
XX  
PS Claim 1; Page 10; 15pp; English.  
XX  
CC This peptide was isolated from the small intestine of a pig. The small



CC inestine is an important endocrine organ and many physiologically active  
CC peptides have been isolated from it. This peptide inhibits the growth of,  
CC and may kill, bacteria, pref. gram negative bacteria. This peptide or its  
CC functional derivatives may be used in human or veterinary medicine for  
CC therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 96; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00037;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPRPPPPFPRLPPRI 16  
| | | | | | | | | | | | | | |  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 13

AAR99121  
ID AAR99121 standard; peptide; 39 AA.

XX  
AC AAR99121;

XX 28-OCT-1996 (first entry)

XX Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.

XX STD; sexually transmitted disease; HIV; human immunodeficiency virus;  
KW herpes simplex virus; HSV; Neisseria gonorrhoeae; Candida; Chlamydia;  
KW magainin; antimicrobial; squalamine.

XX Synthetic.

XX Key Location/Qualifiers  
FH Modified-site 39  
FT /note= "amidated"

XX WO9608270-A2.

XX 21-MAR-1996.

XX 13-SEP-1995; 95WO-US011675.

XX 13-SEP-1994; 94US-00305475.

XX (MAGA-) MAGAININ PHARM INC.

XX Jacob L, Zasloff M, Williams T, Bedi G;

XX WPI; 1996-179725/18.

XX Inhibiting sexually transmitted disease e.g. HIV or herpes simplex - by  
PT administering magainin antimicrobial or squalamine cpd. to inhibit  
PT transmission.

XX Example 1; Page 32; 60pp; English.

XX AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may be  
CC used to treat sexually transmitted diseases (STDs) caused by Chlamydia,  
CC HIV, herpes simplex virus, Neisseria gonorrhoeae or Candida infection.  
CC The peptides inhibit STDs by either killing the infectious organism,  
CC impeding the infection mechanism or interrupting the replication cycle of  
CC the organism. Squalamine (an aminosterol host defence molecule of the dog  
CC fish shark Squalus acanthias) and PGLa (a frog antimicrobial peptide)  
CC analogues may also be useful in inhibiting STD infection and transmission

XX SQ Sequence 39 AA;

Query Match 100.0%; Score 96; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00037;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPRPPPPFPRLPPRI 16  
| | | | | | | | | | | | | | |  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 14

AAR94446  
ID AAR94446 standard; peptide; 39 AA.

XX  
AC AAR94446;

XX 05-NOV-1996 (first entry)

XX Synducin peptide (PR-39) induces syndecan expression.

XX Synducin; induction; expression; syndecan-1; syndecan-4; surface;  
KW mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis;  
KW decubitus; ulcers; keloids; skin burns; ischemic tissues;  
KW hypercoagulation states; prevention; tumour metastasis; restenosis;  
KW inhibition; angiogenesis; proliferation; endothelial.

XX Synthetic.

XX WO9609322-A2.

XX 28-MAR-1996.

XX 22-SEP-1995; 95WO-US012080.

XX 22-SEP-1994; 94US-00310722.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Gallo RL, Bernfield M;

XX WPI; 1996-188401/19.

XX Modulating mesenchymal interaction by administration of synducin - used  
PT in the treatment of wounds, tumours, restenosis, etc.

XX Claim 4; Page 26; 34pp; English.

XX The present peptide is a synducin, which induces the expression of  
CC syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.  
CC fibroblasts and epithelial cells. The 36 N-terminal amino acids of the  
CC peptide were found to be identical to the 36 N-terminal amino acids of PR  
CC -39, a Pro and Arg rich antibacterial peptide previously found in porcine  
CC intestine (WO9222578). Synducins may be used in the treatment of stasis  
CC and decubitus ulcers, keloids, skin burns, ischemic tissues and  
CC hypercoagulation states, prevention of tumour metastasis, restenosis  
CC inhibition and endothelial cell angiogenesis and proliferation induction.  
CC Human microvascular endothelial cells were assayed for syndecan-4  
CC expression following exposure to 5  $\mu$  wound fluid, dbcAMP (1 mM), the  
CC present peptide (10 microM) or a blank, to give respective cell surface  
CC syndecan-4 values (mOD/m in) of approx. 1.75, 1.70, 1.80 and 0.95

XX SQ Sequence 39 AA;

Query Match 100.0%; Score 96; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00037;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPRPPPPFPRLPPRI 16  
| | | | | | | | | | | | | | |  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 15

AAW01446  
ID AAW01446 standard; peptide; 39 AA.

XX  
AC AAW01446;

XX

DT 18-JUN-1997 (first entry)  
XX  
DE Leukocyte O2- production inhibitor peptide PR39.  
XX  
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;  
antimicrobial peptide; small intestine; human; neutrophil; bacteria;  
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;  
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;  
XX tissue damage; oxygen radical; inflammatory disease; therapy.  
OS Synthetic.  
XX  
PN WO9632129-A1.  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-US004674.  
XX  
PR 10-APR-1995; 95US-00419066.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 1996-476842/47.  
XX  
PT Inhibition of leukocyte super:oxide anion prodn. and attraction of  
leukocytes - using peptide(s) partic. based on antimicrobial PR-39.  
XX  
PS Claim 2; Page 26; 45pp; English.  
XX  
CC This sequence represents the proline-arginine rich antimicrobial peptide  
PR39. The PR39 sequence was first isolated from porcine small intestine,  
CC and has also been identified in human and porcine neutrophils. PR39 kills  
CC bacteria by interfering with DNA and/or protein synthesis. PR39 also  
CC induces syndecan expression on mesenchymal cells. Syndecans are important  
CC in wound repair, showing that PR39 can be used in wound repair, as well  
CC as in antibacterial agents. This sequence, and the fragments of it shown  
CC in AAW01447-W01454, can be used in the method of the invention. The  
CC method of the invention is for inhibiting leukocyte superoxide anion (O2-  
CC ) production. The method comprises administering to a leukocyte a peptide  
CC (such as this sequence) capable of inhibiting leukocyte O2- production.  
CC The peptides can be used as medicaments for fighting infection by  
CC attracting leukocytes to a wound site and restricting tissue damage at  
CC the wound site caused by excessive oxygen radicals produced by these  
CC leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 96; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00037;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RPRPPPPFPRLPPRI 16  
| | | | | | | | | | | | | | | |  
Db 11 RPRPPPPFPRLPPRI 26

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 11.9273 Seconds  
(without alignments)  
129.071 Million cell updates/sec

Title: US-10-014-147-5  
Perfect score: 96  
Sequence: 1 RPRPPPPFPRLPPRI 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	96	100.0	172	2	S68232	antimicrobial prot
2	61	63.5	301	2	JQ1663	hybrid proline-ric
3	59	61.5	2584	2	T24158	hypothetical prote
4	59	61.5	2606	2	T24157	hypothetical prote
5	58	60.4	212	2	S57330	cathelin-like anti
6	58	60.4	228	2	S40463	prophenin (PR-2) p
7	56.5	58.9	1137	2	A33507	hypothetical prote
8	56	58.3	736	2	I51691	dishevelled homolo
9	55.5	57.8	1029	2	T30351	mucin-like protein
10	55	57.3	164	2	T26608	hypothetical prote
11	55	57.3	227	2	C69432	hypothetical prote
12	55	57.3	716	2	T26998	hypothetical prote
13	55	57.3	2871	2	A55624	fibrillin-1 precur
14	54	56.2	213	2	T48490	embryo-specific pr
15	54	56.2	302	1	TPCHTC	troponin T, cardia
16	54	56.2	540	2	B47417	insulin receptor-r
17	53	55.2	276	2	B25345	troponin T, cardia
18	53	55.2	276	2	A25345	troponin T, cardia
19	53	55.2	284	2	A28008	troponin T, cardia
20	53	55.2	306	2	I46903	troponin T cardiac
21	53	55.2	588	2	T45564	hypothetical prote
22	53	55.2	903	2	T00074	hypothetical prote
23	52.5	54.7	134	2	D84672	hypothetical prote
24	52	54.2	57	2	S10782	salivary protein P
25	52	54.2	79	1	PJHUSB	proline-rich pepti
26	52	54.2	134	2	JC5572	proline-rich prote
27	52	54.2	199	2	S14981	extensin class I (
28	52	54.2	215	2	S34163	homeotic protein H
29	52	54.2	305	2	JC4525	nucleic acid-bindi

30	52	54.2	329	2	T10064	cytokinin-induced
31	52	54.2	365	2	S43417	RNA/DNA-binding pr
32	52	54.2	389	2	S27200	proline-rich prote
33	52	54.2	411	2	S34164	homeotic protein H
34	52	54.2	417	2	S47539	homeotic protein H
35	52	54.2	1584	2	T18276	protein-tyrosine k
36	52	54.2	1733	1	B45344	probable nuclear a
37	52	54.2	1958	2	B40505	hypothetical prote
38	51.5	53.6	82	2	A41051	spore coat protein
39	51.5	53.6	248	1	JQ1682	infected cell prot
40	51.5	53.6	1560	2	T00080	hypothetical prote
41	51	53.1	278	2	A49266	fas ligand - rat
42	51	53.1	381	2	S52985	cell wall protein
43	51	53.1	401	2	T51407	proline-rich prote
44	51	53.1	464	2	S22697	extensin - Volvox
45	51	53.1	544	2	S44814	F44B9.3 protein -

ALIGNMENTS

RESULT 1

S68232  
antimicrobial protein PR-39 precursor, cathelin-associated - pig  
N;Alternate names: myeloid antibacterial protein PR-39  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S68232; JN0899; I47138; S19563  
R;Zhao, C.; Ganz, T.; Lehrer, R.I.  
FEBS Lett. 376, 130-134, 1995  
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni  
A;Reference number: S68232; MUID:96105365; PMID:7498526  
A;Accession: S68232  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-172 <ZHA>  
A;Cross-references: UNIPROT:P80054; EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g116:  
A;Experimental source: leukocytes  
R;Storici, P.; Zanetti, M.  
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993  
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i  
A;Reference number: JN0899; MUID:94071853; PMID:8250863  
A;Accession: JN0899  
A;Molecule type: mRNA  
A;Residues: 1-20, 'A', 22-172 <STO>  
A;Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101  
A;Experimental source: bone marrow cells  
R;Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bome  
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995  
A;Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami  
A;Reference number: I47138; MUID:95350216; PMID:7624374  
A;Accession: I47138  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <GUD>  
A;Cross-references: EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PID:g1051298  
R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,  
Eur. J. Biochem. 202, 849-854, 1991  
A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of th  
A;Reference number: S19563; MUID:92111534; PMID:1765098  
A;Accession: S19563  
A;Molecule type: protein  
A;Residues: 131-169 <AGE>  
A;Experimental source: intestine  
C;Genetics:  
A;Gene: PR39  
A;Introns: 66/3; 102/3; 126/3  
C;Superfamily: cathelin; cystatin homology  
C;Keywords: amidated carboxyl end; antibacterial  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;22-129/Domain: cystatin homology <CYS>  
F;30-130/Domain: propeptide #status predicted <PRO>  
F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>





Db 199 RPPFFGPPRFPGR 211

RESULT 6

S40463  
prophenin (PF-2) precursor - pig  
N:Alternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S40463; S57331; S68233  
R:Pungercar, J.; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk, FEBS Lett. 336, 284-288, 1993  
A:Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial A:Reference number: S40463; MUID:94085623; PMID:8262247  
A:Accession: S40463  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-228 <PUN>  
A:Cross-references: UNIPROT:P51525; EMBL:X75438; NID:G443812; PIDN:CAA53188.1; PID:G443812  
R:Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V Biol. Chem. Hoppe-Seyler 376, 507-510, 1995  
A:Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte A:Reference number: S57330; MUID:96042752; PMID:7576250  
A:Accession: S57331  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-228 <STR>  
R:Zhao, C.; Ganz, T.; Lehrer, R.I. FEBS Lett. 376, 130-134, 1995  
A:Title: Structures of genes for two cathelin-associated antimicrobial peptides: propher A:Reference number: S68232; MUID:96105365; PMID:7498526  
A:Accession: S68233  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-228 <ZHA>  
A:Cross-references: EMBL:X89202; NID:G1165148; PIDN:CAA61488.1; PID:G1165149  
C:Genetics:  
A:Introns: 66/3; 102/3; 126/3  
C:Superfamily: cathelin; cystatin homology  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:22-129/Domain: cystatin homology <CYS>  
F:30-228/Product: prophenin (PF-2) #status predicted <MAT>

Query Match 60.4%; Score 58; DB 2; Length 228;  
Best Local Similarity 76.9%; Pred. No. 2.9;  
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 3 RPPFFPRLPRLPPR 15

Db 215 RPPFFGPPRFPGR 227

RESULT 7

A33507  
hypothetical protein DUC-1 - human  
C:Species: Homo sapiens (man)  
C>Date: 08-Dec-1989 #sequence\_revision 08-Dec-1989 #text\_change 09-Jul-2004  
C:Accession: A33507  
R:Fujii, H.; Shimada, T. J. Biol. Chem. 264, 10057-10064, 1989  
A:Title: Isolation and characterization of cDNA clones derived from the divergently tran A:Reference number: A33507; MUID:89255490; PMID:2722860  
A:Accession: A33507  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1137 <FUJ>  
A:Cross-references: UNIPROT:P20585; GB:J04810; NID:G181841; PIDN:AAB47281.1; PID:G181842

Query Match 58.9%; Score 56.5; DB 2; Length 1137;  
Best Local Similarity 62.5%; Pred. No. 21;  
Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 PRPP-PFFPRLPRLP 16

Db 64 PAPPAPAPPQLPPHV 79

RESULT 8

I51691  
dishevelled homolog - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I51691  
R:Sokol, S.Y.; Klingensmith, J.; Perrimon, N.; Itoh, K. Development 121, 1637-1647, 1995  
A:Title: Dorsalizing and neuralizing properties of Xdsh, a maternally expressed Xenopus i A:Reference number: I51691; MUID:95324391; PMID:7600981  
A:Accession: I51691  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-736 <SOK>  
A:Cross-references: UNIPROT:P51142; EMBL:U31552; NID:G945109; PIDN:AAB00688.1; PID:G94511  
C:Genetics:  
A:Gene: Xdsh  
F:260-336/Domain: GLGF domain homology <GLG4>

Query Match 58.3%; Score 56; DB 2; Length 736;  
Best Local Similarity 64.3%; Pred. No. 16;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLP 14

Db 98 RPEPPPPVPPPIPP 111

RESULT 9

T30351  
mucin-like protein - Lymantria dispar nuclear polyhedrosis virus  
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T30351  
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrn Virology 253, 17-34, 1999  
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di A:Reference number: Z20836; MUID:99124785; PMID:9887315  
A:Accession: T30351  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1029 <KUZ>  
A:Cross-references: UNIPROT:Q9YMX0; EMBL:AF081810; PIDN:AAC70189.1

Query Match 57.8%; Score 55.5; DB 2; Length 1029;  
Best Local Similarity 52.4%; Pred. No. 25;  
Matches 11; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 1 RPR-----PPPPFPRLP 14

Db 927 RPRYSQQPPPPPPFPFP 947

RESULT 10

T26608  
hypothetical protein Y37A1B.2a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26608  
R:McMurray, A. submitted to the EMBL Data Library, June 1998  
A:Reference number: Z20245  
A:Accession: T26608  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-164 <WIL>  
A:Cross-references: UNIPROT:Q9XXG3; EMBL:AL023835; PIDN:CAA19486.1; GSPDB:GN00022; CESP: A:Experimental source: clone Y37A1B  
C:Genetics:



A;Gene: CESP:Y37A1B.2a  
A;Map position: 4  
A;Introns: 32/3; 66/3

Query Match 57.3%; Score 55; DB 2; Length 164;  
Best Local Similarity 75.0%; Pred. No. 4.8;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 RPPPPFFPPRLPP 14  
||||| ||| |||||  
Db 63 RPPPVLPPLPP 74

RESULT 11  
C69432  
hypothetical protein AF1460 - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: C69432  
R;Kienk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Godek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: C69432  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-227 <KLE>  
A;Cross-references: UNIPROT:O28812; GB:AE001002; GB:AE000782; NID:g2689325; PIDN:AAB8979

Query Match 57.3%; Score 55; DB 2; Length 227;  
Best Local Similarity 72.7%; Pred. No. 6.6;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPPFFPPRLPP 14  
||| ||| |||  
Db 2 PPPMIPPKLPP 12

RESULT 12  
T26998  
hypothetical protein Y48B6A.6 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T26998  
R;Wall, M.  
submitted to the EMBL Data Library, September 1999  
A;Reference number: Z20297  
A;Accession: T26998  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-716 <WIL>  
A;Cross-references: UNIPROT:Q9U2A6; EMBL:AL110490; NID:e1542263; PIDN:CAB54442.1; CESP:Y  
A;Experimental source: clone Y48B6A  
C;Genetics:  
A;Gene: CESP:Y48B6A.6  
A;Introns: 38/3; 196/3; 437/2; 460/3; 518/1; 617/3; 673/3

Query Match 57.3%; Score 55; DB 2; Length 716;  
Best Local Similarity 69.2%; Pred. No. 20;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PRPPFFPPRLPP 14  
| ||| ||| |||  
Db 197 PPPPTSPPLPP 209

RESULT 13  
A55624  
fibrillin-1 precursor - mouse

C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A55624  
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez, f  
J. Biol. Chem. 270, 1798-1806, 1995  
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin ger  
A;Reference number: A55624; MUID:95130561; PMID:7829516  
A;Accession: A55624  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2871 <YIN>  
A;Cross-references: UNIPROT:Q61554; GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510  
C;Genetics:  
A;Gene: Fbn-1  
C;Superfamily: fibrillin; EGF homology  
F;1201-1236/Domain: EGF homology <EGF>

Query Match 57.3%; Score 55; DB 2; Length 2871;  
Best Local Similarity 58.8%; Pred. No. 81;  
Matches 10; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 2 PRPPP--FFPPRLPPRI 16  
||||| :| |||||  
Db 428 PRPPEVLYPSREPPRV 444

RESULT 14  
T48490  
embryo-specific protein 3 (ATS3) - Arabidopsis thaliana  
N;Alternate names: protein T28J14.130  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48490  
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Len  
submitted to the Protein Sequence Database, April 2000  
A;Reference number: Z24493  
A;Accession: T48490  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-213 <BEV>  
A;Cross-references: UNIPROT:Q9LYP6; EMBL:AL163652  
A;Experimental source: cultivar Columbia; BAC clone T28J14  
C;Genetics:  
A;Map position: 5  
A;Introns: 28/3; 65/3  
A;Note: T28J14.130

Query Match 56.2%; Score 54; DB 2; Length 213;  
Best Local Similarity 72.7%; Pred. No. 8.1;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPPFFPPRLPP 14  
||| ||| |||  
Db 160 PPPHFPPEFPP 170

RESULT 15  
TPCHTC  
troponin T, cardiac muscle, embryonic splice form - chicken  
N;Contains: cardiac muscle troponin T, adult splice form  
C;Species: Gallus gallus (chicken)  
C;Date: 28-Aug-1985 #sequence\_revision 12-Apr-1996 #text\_change 09-Jul-2004  
C;Accession: A25373; A03086  
R;Cooper, T.A.; Ordahl, C.P.  
J. Biol. Chem. 260, 11140-11148, 1985  
A;Title: A single cardiac troponin T gene generates embryonic and adult isoforms via deve  
A;Reference number: A25373; MUID:85289327; PMID:2993302  
A;Accession: A25373  
A;Molecule type: mRNA  
A;Residues: 1-302 <COO>  
A;Cross-references: UNIPROT:P02642; GB:M10013; NID:g212783; PIDN:AAA49099.1; PID:g212784  
R;Cooper, T.A.; Ordahl, C.P.  
Science 226, 979-982, 1984

A;Title: A single troponin T gene regulated by different programs in cardiac and skeletal  
A;Reference number: A03086; MUID:85065747; PMID:6095446  
A;Accession: A03086  
A;Molecule type: mRNA  
A;Residues: 68-302 <CO2>  
A;Cross-references: NID:g212781; PIDN:AAA49098.1; PID:g212782  
C;Comment: This protein, found in adult cardiac muscle and transiently in embryonic skeletal muscle. Down-regulation of the protein in the late stages of skeletal muscle and skeletal muscle. Down-regulation of the protein in the late stages of skeletal muscle and skeletal muscle. Down-regulation of the protein in the late stages of skeletal muscle and skeletal muscle.  
C;Superfamily: troponin T  
C;Keywords: alternative splicing; cardiac muscle; differentiation; heart; muscle; phosph  
F;1-302/Product: troponin T, cardiac muscle, embryonic splice form #status predicted <MA  
F;1-22,33-302/Product: troponin T, cardiac muscle, adult splice form #status predicted <

Query Match 56.2%; Score 54; DB 1; Length 302;  
Best Local Similarity 50.0%; Pred. No. 11;  
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
:|:| | | :|:|  
Db 78 KPKPKPFMPNLPVKI 93

Search completed: October 26, 2005, 05:19:59  
Job time : 12.9273 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:52:03 ; Search time 55.4182 Seconds  
(without alignments)  
147.844 Million cell updates/sec

Title: US-10-014-147-5  
Perfect score: 96  
Sequence: 1 RPRPPPPPPRPPRI 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	96	100.0	172	1	PR39_PIG	P80054 sus scrofa
2	63	65.6	378	1	FBSH_MOUSE	Q8r089 mus musculus
3	61	63.5	103	2	Q99FW9	Q99fw9 human papil
4	61	63.5	301	2	Q41848	Q41848 zea mays (m
5	61	63.5	2133	2	Q7PQG9	Q7pgg9 anopheles g
6	60	62.5	328	2	Q96F80	Q96f80 homo sapien
7	60	62.5	378	2	Q8WVN3	Q8wvn3 homo sapien
8	60	62.5	508	2	Q99LH0	Q99lh0 mus musculus
9	60	62.5	513	2	Q8BWX7	Q8bwx7 mus musculus
10	60	62.5	520	2	Q9H077	Q9h077 homo sapien
11	60	62.5	545	2	Q9DBB2	Q9dbb2 mus musculus
12	60	62.5	581	2	Q9D824	Q9d824 mus musculus
13	60	62.5	594	2	Q6UN15	Q6un15 homo sapien
14	59	61.5	347	1	DTX3_HUMAN	Q8n9i9 homo sapien
15	59	61.5	347	1	DTX3_MOUSE	Q80v91 mus musculus
16	59	61.5	1395	2	Q7SC01	Q7sc01 neurospora
17	59	61.5	2584	2	Q9TW88	Q9tw88 caenorhabdi
18	59	61.5	2606	2	Q21920	Q21920 caenorhabdi
19	58	60.4	105	2	Q6ETT6	Q6ett6 oryza sativ
20	58	60.4	139	2	Q6H843	Q6h843 oryza sativ
21	58	60.4	150	2	Q67VV4	Q67vv4 oryza sativ
22	58	60.4	150	2	Q6Z4P0	Q6z4p0 oryza sativ
23	58	60.4	212	1	PF11_PIG	P51524 sus scrofa
24	58	60.4	228	1	PF12_PIG	P51525 sus scrofa
25	58	60.4	586	2	Q63ZL7	Q63zl7 xenopus lae
26	58	60.4	806	2	Q6CQH5	Q6cqh5 kluyveromyc
27	57	59.4	187	2	Q9FG86	Q9fg86 arabidopsis
28	57	59.4	228	2	Q6Z8Z0	Q6z8z0 oryza sativ
29	57	59.4	333	2	Q9XI23	Q9xi23 oryza sativ
30	57	59.4	548	2	Q6ESK7	Q6esk7 oryza sativ
31	57	59.4	625	2	Q8S9B5	Q8s9b5 volvox cart

32	57	59.4	825	2	Q7S9H3	Q7s9h3 neurospora
33	56.5	58.9	541	2	Q7RYV7	Q7ryv7 neurospora
34	56.5	58.9	1137	1	MSH3_HUMAN	P20585 homo sapien
35	56.5	58.9	1140	2	Q86UQ6	Q86uq6 homo sapien
36	56	58.3	165	2	Q6ZL86	Q6z186 oryza sativ
37	56	58.3	196	2	Q7XII7	Q7xi17 oryza sativ
38	56	58.3	372	1	FBSH_HUMAN	Q9hah7 homo sapien
39	56	58.3	484	2	Q8ILQ0	Q8ilq0 plasmodium
40	56	58.3	721	2	Q6NTP8	Q6ntp8 xenopus lae
41	56	58.3	736	1	DVL2_XENLA	P51142 xenopus lae
42	55.5	57.8	1029	2	Q9VMX0	Q9ymx0 lymantria d
43	55	57.3	164	2	Q9XXG3	Q9xxg3 caenorhabdi
44	55	57.3	205	2	Q9FI79	Q9fi79 arabidopsis
45	55	57.3	227	1	YE60_ARCFU	O28812 archaeoglob

ALIGNMENTS

RESULT 1  
PR39\_PIG  
ID PR39\_PIG STANDARD; PRT; 172 AA.  
AC P80054; Q9TR84;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antibacterial protein PR-39 precursor.  
GN Name=PR39;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
SEQUENCE FROM N.A.  
RP MEDLINE=95350216; PubMed=7624374;  
RX Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,  
RA Andersson L., Boman H.G.;  
RT "Structure of the gene for porcine peptide antibiotic PR-39, a  
RT cathelin gene family member: comparative mapping of the locus for the  
RT human peptide antibiotic FALL-39.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).  
RN [2]  
SEQUENCE FROM N.A.  
RP TISSUE=Bone marrow;  
RC MEDLINE=94071853; PubMed=8250863;  
RX Storici P., Zanetti M.;  
RT "A cDNA derived from pig bone marrow cells predicts a sequence  
RT identical to the intestinal antibacterial peptide PR-39.";  
RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).  
RN [3]  
SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RC MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;  
RX Zhao C., Ganz T., Lehrer R.I.;  
RA "Structures of genes for two cathelin-associated antimicrobial  
RT peptides: prophenin-2 and PR-39.";  
RL FEBS Lett. 376:130-134(1995).  
RN [4]  
SEQUENCE OF 131-169.  
RP TISSUE=Intestine;  
RC MEDLINE=92111534; PubMed=1765098;  
RX Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,  
RA Mutt V., Joernvall H.;  
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new  
RT member of the family of proline-arginine-rich antibacterial  
RT peptides.";  
RL Eur. J. Biochem. 202:849-854(1991).  
RN [5]  
SEQUENCE OF 131-164, AND FUNCTION.  
RP TISSUE=Neutrophils;  
RC MEDLINE=95088504; PubMed=7996056;  
RX Shi J., Ross C.R., Chengappa M.M., Blecha F.;  
RA "Identification of a proline-arginine-rich antibacterial peptide from

RT neutrophils that is analogous to PR-39, an antibacterial peptide from  
RT the small intestine.";  
RL J. Leukoc. Biol. 56:807-811(1994).  
CC -!- FUNCTION: Exerts a potent antimicrobial activity against both  
CC E.coli and B.megaterium.  
CC -!- TISSUE SPECIFICITY: Small intestine and bone marrow.  
CC -!- SIMILARITY: Belongs to the cathelicidin family.  
CC -----  
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CC -----  
CC EMBL; X87236; CAA60682.1; --  
DR EMBL; L23825; AAA31109.1; --  
DR EMBL; X89201; CAA61487.1; --  
DR PIR; S68232; S68232.  
DR HSSP; P32196; 1KWI.  
DR InterPro; IPR001894; Cathelicidin.  
DR Pfam; PF00666; Cathelicidins; 1.  
DR ProDom; PD001838; Cathelicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
KW Amidation; Antibiotic; Direct protein sequencing;  
KW Pyrrolidone carboxylic acid; Signal.  
FT SIGNAL 1 29 Potential.  
FT PROPEP 30 130  
FT CHAIN 131 169 Antibacterial protein PR-39.  
FT MOD\_RES 30 30 Pyrrolidone carboxylic acid (By  
FT similarity).  
FT DISULFID 85 96 By similarity.  
FT DISULFID 107 124 By similarity.  
FT MOD\_RES 169 169 Proline amide (G-170 provides amide  
FT group).  
FT CONFLICT 21 21 G -> A (in Ref. 2).  
FT CONFLICT 29 29 A -> T (in Ref. 1).  
FT CONFLICT 90 91 RQ -> QR (in Ref. 1).  
FT CONFLICT 117 119 IHS -> NDP (in Ref. 1).  
FT CONFLICT 157 157 P -> I (in Ref. 5).  
SQ SEQUENCE 172 AA; 19476 MW; 994B792798C0E133 CRC64;  
  
Query Match 100.0%; Score 96; DB 1; Length 172;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RPRPPPPFPRLPPRI 16  
Db 141 RPRPPPPFPRLPPRI 156  
  
RESULT 2  
FBSH\_MOUSE STANDARD; PRT; 378 AA.  
AC Q8R089;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Probable fibrosin 1 long transcript protein.  
GN Name=Fbs1; Synonyms=Fbs;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thymus;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- CAUTION: This CDS has been thought to correspond to fibrosin 1,  
CC but the fibrosin 1 sequence which has been characterized (AC  
CC Q60791) is found in the 3'UTR of these cDNAs. They could  
CC correspond to alternatively spliced isoforms.  
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CC -----  
CC EMBL; AK037952; -; NOT ANNOTATED\_CDS.  
DR EMBL; BC027193; AAH27193.1; -.  
DR MGD; MGI:104648; Fbs1.  
FT DOMAIN 223 246 Ala-rich.  
FT DOMAIN 260 373 Pro-rich.  
FT CONFLICT 195 195 A -> T (in Ref. 1).  
SQ SEQUENCE 378 AA; 39456 MW; 4C3FAF0D4AC29E69 CRC64;  
  
Query Match 65.6%; Score 63; DB 1; Length 378;  
Best Local Similarity 73.3%; Pred. No. 11;



Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPR 15  
|||||:|:|  
Db 259 RPRPPPFGLPSLPER 273

RESULT 3  
Q99FW9 PRELIMINARY; PRT; 103 AA.  
AC Q99FW9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE Putative E4 protein.  
OS Human papillomavirus type 84.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=150546;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21066735; PubMed=11145894; DOI=10.1006/viro.2000.0716;  
RA Terai M., Burk R.D.;  
RT "Complete nucleotide sequence and analysis of a novel human  
RT papillomavirus (HPV 84) genome cloned by an overlapping PCR method.";  
RL Virology 279:109-115(2001).  
DR EMBL; AF293960; AAK09275.1; -.  
DR InterPro; IPR003861; Papilloma\_E4.  
DR Pfam; PF02711; Pap\_E4; 1.  
SQ SEQUENCE 103 AA; 11162 MW; 2C32F1FD23337E55 CRC64;

Query Match 63.5%; Score 61; DB 2; Length 103;  
Best Local Similarity 73.3%; Pred. No. 5.1;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPR 15  
|||||:|:|  
Db 31 RPPPPPSAAPRLPPR 45

RESULT 4  
Q41848 PRELIMINARY; PRT; 301 AA.  
AC Q41848;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Prolin rich protein.  
GN Name=PRP;  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W64A;  
RX MEDLINE=92361259; PubMed=1498600;  
RA Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;  
RT "A maize embryo-specific gene encodes a proline-rich and hydrophobic  
RT protein.";  
RL Plant Cell 4:413-423(1992).  
DR EMBL; X60432; CAA42959.1; -.  
DR PIR; JQ1663; JQ1663.  
DR HSSP; P24337; IHYP.  
DR InterPro; IPR003612; AAI.  
DR Pfam; PF00234; Tryp\_alpha\_amyl; 1.  
DR SMART; SM00499; AAI; 1.  
SQ SEQUENCE 301 AA; 31647 MW; 884EB70854D28C2E CRC64;

Query Match 63.5%; Score 61; DB 2; Length 301;  
Best Local Similarity 64.3%; Pred. No. 15;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPP 14  
|||||:|:|  
Db 179 RPSPPPYVPYVPP 192

RESULT 5  
Q7PQG9 PRELIMINARY; PRT; 2133 AA.  
AC Q7PQG9;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ENSANGP0000020211 (Fragment).  
GN Name=ENSANGG0000017722;  
OS Anopheles gambiae str. PEST.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
OX NCBI\_TaxID=180454;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PEST;  
RA Anopheles Genome Sequencing Consortium;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAAB01008888; EAA08848.2; -.  
DR HSSP; P01130; 1D2J.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR009030; Grow\_fac\_recept.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR002172; LDL\_receptor\_A.  
DR Pfam; PF00047; Ig; 2.  
DR Pfam; PF00052; Laminin\_B; 3.  
DR Pfam; PF00053; Laminin\_EGF; 4.  
DR Pfam; PF00057; Ldl\_recept\_a; 5.  
DR PRINTS; PR00261; LDLRECEPTOR.  
DR ProDom; PD003031; Laminin\_B; 3.  
DR PROSITE; PS00022; EGF\_1; 7.  
DR PROSITE; PS01186; EGF\_2; 4.  
DR PROSITE; PS50835; IG\_LIKE; 9.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 7.  
DR PROSITE; PS01209; LDLRA\_1; 5.  
DR PROSITE; PS50068; LDLRA\_2; 5.  
KW Laminin EGF-like domain.  
FT NON\_TER 1  
FT NON\_TER 2133 2133  
SQ SEQUENCE 2133 AA; 235646 MW; 16E7ADC733959F6C CRC64;

Query Match 63.5%; Score 61; DB 2; Length 2133;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RPPPPFPRLPP 14  
|||||:|:|  
Db 1941 RPPSYVPRLPP 1952

RESULT 6  
Q96F80 PRELIMINARY; PRT; 328 AA.  
AC Q96F80;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Similar to RIKEN cDNA 1300019H17 gene (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011543; AAH11543.1; -.
FT NON TER 1
SQ SEQUENCE 328 AA; 37615 MW; 38472A76B3E8A1B9 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 328;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFPPLPP 14
Db 89 KPPFPFPFGAPP 100

RESULT 7
Q8WVN3
ID Q8WVN3 PRELIMINARY; PRT; 378 AA.
AC Q8WVN3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fip1l1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003263; AAH03263.1; -.
DR MGD; MGI:1914149; Fip1l1.
DR InterPro; IPR007854; Fip1.
DR Pfam; PF05182; Fip1; 1.
SQ SEQUENCE 378 AA; 40834 MW; 1B699B114C9560D4 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 378;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFPPLPP 14
Db 340 KPPFPFPFGAPP 351

us-10-014-147-5.rup
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RESULT 8
Q99LH0
ID Q99LH0 PRELIMINARY; PRT; 508 AA.
AC Q99LH0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fip1l1 protein.
GN Name=Fip1l1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003263; AAH03263.1; -.
DR MGD; MGI:1914149; Fip1l1.
DR InterPro; IPR007854; Fip1.
DR Pfam; PF05182; Fip1; 1.
SQ SEQUENCE 508 AA; 55796 MW; 01BF436596282ED4 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 508;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFPPLPP 14
Db 354 KPPFPFPFGAPP 365

RESULT 9
Q8BWV7
ID Q8BWV7 PRELIMINARY; PRT; 513 AA.
AC Q8BWV7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
enriched library, clone:C530020P17 product:weakly similar to TOMATO
CELL WALL HRGP (HYDROXPROLINE-RICH GLYCOPROTEIN) (Fragment).
GN Name=Fip1l1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;  
RA The FANTOM Consortium;  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK049672; BAC33867.1; -.  
DR MGD; MGI:1914149; Fip1l1.  
DR InterPro; IPR007854; Fip1.  
DR Pfam; PF05182; Fip1; 1.  
FT NON TER 513 513  
SQ SEQUENCE 513 AA; 57835 MW; CC9CD61F7A0C2062 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 513;  
Best Local Similarity 75.0%; Pred. No. 33;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFPRLPP 14  
Db :|||||

RESULT 10  
Q9H077 PRELIMINARY; PRT; 520 AA.  
ID Q9H077;  
AC Q9H077;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein DKFZp586K0717.  
GN Name=DKFZp586K0717;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus;  
RG The German cDNA Consortium;  
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
Fobo G., Han M., Wiemann S.;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL136910; CAB66844.1; -.  
DR Genew; HGNC:19124; FIP1L1.  
DR InterPro; IPR007854; Fip1.  
DR Pfam; PF05182; Fip1; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 520 AA; 58375 MW; 55D48285A046A783 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 520;  
Best Local Similarity 75.0%; Pred. No. 33;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFPRLPP 14  
Db :|||||

RESULT 11  
Q9DBB2 PRELIMINARY; PRT; 545 AA.  
ID Q9DBB2  
AC Q9DBB2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mus musculus adult male liver cDNA, RIKEN full-length enriched  
DE library, clone:1300019H17 product:weakly similar to TOMATO CELL WALL  
DE HRGP (HYDROXPROLINE-RICH GLYCOPROTEIN).  
GN Name=Fip1l1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RA The FANTOM Consortium;  
RT "Analysis of the mouse transcriptome based on functional annotation of



RT 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

RN {4}

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN {5}

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN {6}

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

RA Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBDJ databases.

DR EMBL; AK005061; BAB23785.1; -.

DR MGD; MGI:1914149; Fip1l1.

DR InterPro; IPR007854; Fip1.

DR Pfam; PF05182; Fip1; 1.

SQ SEQUENCE 545 AA; 61059 MW; D8C65A7E20CA0985 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 545;

Best Local Similarity 75.0%; Pred. No. 35;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFFPRLPP 14

Db 295 KPPPPFFPPGAPP 306

RESULT 12

Q9D824 PRELIMINARY; PRT; 581 AA.

AC Q9D824;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Mus musculus adult male small intestine cDNA, RIKEN full-length

DE enriched library, clone:2010310H23 product:weakly similar to TOMATO

DE CELL WALL HRGP (HYDROXYPROLINE-RICH GLYCOPROTEIN).

GN Name=Fip1l1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN {2}

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/350555500;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN {3}

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN {4}

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN {5}

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN {6}

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

RA Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBDJ databases.

DR EMBL; AK008561; BAB25745.1; -.

DR MGD; MGI:1914149; Fip1l1.

DR InterPro; IPR007854; Fip1.

DR Pfam; PF05182; Fip1; 1.

SQ SEQUENCE 581 AA; 64958 MW; 2E8D6DF558168035 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 581;

Best Local Similarity 75.0%; Pred. No. 37;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPPPPFFPRLPP 14

Db 331 KPPPPFFPPGAPP 342

RESULT 13





Db 139 PPPPPPLPPPLPRL 153

RESULT 15

DTX3 MOUSE

ID DTX3 MOUSE STANDARD; PRT; 347 AA.

AC Q80V91; Q9ER06;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Deltex protein 3 (Deltex-3) (Deltex3) (mDTX3).

GN Name=Dtx3;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MULTIMERIZATION.

RX MEDLINE=21123790; PubMed=11226752; DOI=10.1016/S0736-5748(00)00071-X;

RA Kishi N., Tang Z., Maeda Y., Hirai A., Mo R., Ito M., Suzuki S., Nakao K., Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S., Okano H., Matsuno K.;

RA "Murine homologs of dltex define a novel gene family involved in vertebrate Notch signaling and neurogenesis.";

RL Int. J. Dev. Neurosci. 19:21-35(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Breast tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Regulator of Notch signaling, a signaling pathway involved in cell-cell communications that regulates a broad spectrum of cell-fate determinations. Probably acts both as a positive and negative regulator of Notch, depending on the developmental and cell context. Functions as an ubiquitin ligase protein in vitro, suggesting that it may regulate the Notch pathway via some ubiquitin ligase activity (By similarity).

CC -!- SUBUNIT: Homomultimer. May form a heteromultimer with other members of the Deltex family. Interacts with NOTCH1.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -!- TISSUE SPECIFICITY: Strongly expressed in testis and brain. Weakly expressed in kidney.

CC -!- DEVELOPMENTAL STAGE: In the CNS, it is expressed in the developing neural tube starting from E10.5 in the spinal cord and around E11.5 in the telencephalon. Expressed ubiquitously throughout the spinal cord and telencephalon during neurogenesis. Expressed throughout the developing retina at E15.5. Not expressed in the somite or presomite during somitogenesis. Expressed slightly later than Dtx2.

CC -!- SIMILARITY: Belongs to the Deltex family.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

CC -!- CAUTION: Ref.2 sequence differs from that shown due to a chimeric cDNA.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL; AB015425; BAB18942.1; -

DR EMBL; BC044779; AAH44779.1; ALT\_SEQ.

DR MGD; MGI:2135752; Dtx3.

DR InterPro; IPR011046; WD40\_like.

DR InterPro; IPR001841; Znf\_Ring.

DR Pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS00518; ZF\_RING\_1; 1.

DR PROSITE; PS50089; ZF\_RING\_2; 1.

KW Metal-binding; Notch\_signaling pathway; Zinc; Zinc-finger.

FT ZN FING 164 205 RING-type.

FT DOMAIN 115 151 Pro-rich.

SQ SEQUENCE 347 AA; 37982 MW; 2368BB96D49967AD CRC64;

Query Match 61.5%; Score 59; DB 1; Length 347;

Best Local Similarity 66.7%; Pred. No. 29;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PRPPPPPPRLPPRI 16

Db 139 PPPPPPLPPPLPRL 153

Search completed: October 26, 2005, 05:18:35

Job time : 57.4182 secs

GenCore version.5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 16.4364 Seconds  
(without alignments)  
72.667 Million cell updates/sec

Title: US-10-014-147-5

Perfect score: 96

Sequence: 1 RPRPPPPFPRLPPRI 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	16	3 US-09-024-975-3	Sequence 3, Appli
2	96	100.0	16	4 US-08-930-777A-5	Sequence 5, Appli
3	96	100.0	23	4 US-08-930-777A-3	Sequence 3, Appli
4	96	100.0	26	2 US-08-419-066-2	Sequence 2, Appli
5	96	100.0	26	3 US-09-024-975-2	Sequence 2, Appli
6	96	100.0	26	4 US-08-930-777A-2	Sequence 2, Appli
7	96	100.0	38	4 US-09-739-535-1	Sequence 1, Appli
8	96	100.0	39	1 US-08-162-052-1	Sequence 1, Appli
9	96	100.0	39	1 US-08-310-722-1	Sequence 1, Appli
10	96	100.0	39	2 US-08-419-066-1	Sequence 1, Appli
11	96	100.0	39	2 US-08-728-333-1	Sequence 1, Appli
12	96	100.0	39	3 US-09-024-975-1	Sequence 1, Appli
13	96	100.0	39	4 US-08-930-777A-1	Sequence 1, Appli
14	96	100.0	39	5 PCT-US95-12080-1	Sequence 1, Appli
15	63	65.6	311	3 US-09-179-558-66	Sequence 66, Appl
16	63	65.6	311	4 US-09-722-825-66	Sequence 66, Appl
17	63	65.6	311	4 US-09-722-487-66	Sequence 66, Appl
18	63	65.6	311	4 US-09-722-708-66	Sequence 66, Appl
19	60	62.5	521	4 US-09-149-476-392	Sequence 392, App
20	59	61.5	313	3 US-08-957-351-9	Sequence 9, Appli
21	57	59.4	15	4 US-08-930-777A-6	Sequence 6, Appli
22	57	59.4	19	4 US-08-930-777A-4	Sequence 4, Appli
23	56.5	58.9	1137	4 US-09-538-092-968	Sequence 968, App
24	55	57.3	78	1 US-08-487-359-5	Sequence 5, Appli
25	55	57.3	78	1 US-08-487-359-7	Sequence 7, Appli
26	55	57.3	78	1 US-08-222-798A-5	Sequence 5, Appli
27	55	57.3	78	1 US-08-222-798A-7	Sequence 7, Appli

28	55	57.3	79	1	US-08-487-359-1	Sequence 1, Appli
29	55	57.3	79	1	US-08-487-359-2	Sequence 2, Appli
30	55	57.3	79	1	US-08-487-359-3	Sequence 3, Appli
31	55	57.3	79	1	US-08-487-359-8	Sequence 8, Appli
32	55	57.3	79	1	US-08-222-798A-1	Sequence 1, Appli
33	55	57.3	79	1	US-08-222-798A-2	Sequence 2, Appli
34	55	57.3	79	1	US-08-222-798A-3	Sequence 3, Appli
35	55	57.3	79	1	US-08-222-798A-8	Sequence 8, Appli
36	55	57.3	107	4	US-09-252-991A-32013	Sequence 32013, A
37	55	57.3	442	4	US-09-248-796A-21400	Sequence 21400, A
38	54	56.2	511	4	US-09-107-433-2904	Sequence 2904, Ap
39	54	56.2	674	3	US-08-893-852A-1	Sequence 1, Appli
40	53	55.2	186	4	US-09-489-039A-8182	Sequence 8182, Ap
41	52	54.2	79	1	US-08-487-359-4	Sequence 4, Appli
42	52	54.2	79	1	US-08-222-798A-4	Sequence 4, Appli
43	52	54.2	97	4	US-09-489-039A-10835	Sequence 10835, A
44	52	54.2	433	4	US-09-949-016-6497	Sequence 6497, Ap
45	52	54.2	802	4	US-09-823-240A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-024-975-3  
; Sequence 3, Application US/09024975  
; Patent No. 6133233  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, CHRISTOPHER R.  
; APPLICANT: BLECHA, FRANK  
; APPLICANT: SHI, JISHU  
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
; STREET: 2405 GRAND BLVD., SUITE 400  
; CITY: KANSAS CITY  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/024,975  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/802,306  
; APPLICATION NUMBER: 18-FEB-1997  
; FILING DATE: 18-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COLLINS, JOHN M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 25585-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 816/474-9050  
; TELEFAX: 816/474-9057  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-024-975-3

Query Match 100.0%; Score 96; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
|||||

Db 1 RPRPPPPPPRLPPRI 16

RESULT 2

US-08-930-777A-5

; Sequence 5, Application US/08930777A

; Patent No. 6713605

; GENERAL INFORMATION:

; APPLICANT: Blecha, Frank

; APPLICANT: Shi, Jishu

; TITLE OF INVENTION: Synthetic Antimicrobial Peptide

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hovey, Williams, Timmons & Collins

; STREET: 2405 Grand Blvd., Ste. 400

; CITY: Kansas City

; STATE: Missouri

; COUNTRY: U.S.A.

; ZIP: 64108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/930,777A

; FILING DATE: October 8, 1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/04674

; FILING DATE: April 10, 1996

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Collins, John M.

; REGISTRATION NUMBER: 26,262

; REFERENCE/DOCKET NUMBER: 23625-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (816) 474-9050

; TELEFAX: (816) 474-9057

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-930-777A-5

Query Match 100.0%; Score 96; DB 4; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRLPPRI 16

Db 1 RPRPPPPPPRLPPRI 16

RESULT 3

US-08-930-777A-3

; Sequence 3, Application US/08930777A

; Patent No. 6713605

; GENERAL INFORMATION:

; APPLICANT: Blecha, Frank

; APPLICANT: Shi, Jishu

; TITLE OF INVENTION: Synthetic Antimicrobial Peptide

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hovey, Williams, Timmons & Collins

; STREET: 2405 Grand Blvd., Ste. 400

; CITY: Kansas City

; STATE: Missouri

; COUNTRY: U.S.A.

; ZIP: 64108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/930,777A

; FILING DATE: October 8, 1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/04674

; FILING DATE: April 10, 1996

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Collins, John M.

; REGISTRATION NUMBER: 26,262

; REFERENCE/DOCKET NUMBER: 23625-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (816) 474-9050

; TELEFAX: (816) 474-9057

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-930-777A-3

Query Match 100.0%; Score 96; DB 4; Length 23;

Best Local Similarity 100.0%; Pred. No. 2.9e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRLPPRI 16

Db 8 RPRPPPPPPRLPPRI 23

RESULT 4

US-08-419-066-2

; Sequence 2, Application US/08419066

; Patent No. 5830993

; GENERAL INFORMATION:

; APPLICANT: Blecha, Frank

; APPLICANT: Shi, Jishu

; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &

; ADDRESSEE: Collins

; STREET: 2405 Grand Boulevard, Suite 400

; CITY: Kansas City

; STATE: Missouri

; COUNTRY: U.S.A.

; ZIP: 64108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/419,066

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Collins, John M.

; REGISTRATION NUMBER: 26262

; REFERENCE/DOCKET NUMBER: 23625

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (816) 474-9050

; TELEFAX: (816) 474-9057

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 amino acids

; TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-419-066-2

Query Match 100.0%; Score 96; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRRLPPRI 16  
| | | | | | | | | |  
Db 11 RPRPPPPPPRRLPPRI 26

RESULT 5  
US-09-024-975-2  
Sequence 2, Application US/09024975  
Patent No. 6133233  
GENERAL INFORMATION:  
APPLICANT: ROSS, CHRISTOPHER R.  
APPLICANT: BLECHA, FRANK  
APPLICANT: SHI, JISHU  
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
STREET: 2405 GRAND BLVD., SUITE 400  
CITY: KANSAS CITY  
STATE: MO  
COUNTRY: USA  
ZIP: 64108

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/024,975  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/802,306  
FILING DATE: 18-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: COLLINS, JOHN M.  
REGISTRATION NUMBER: 26,262  
REFERENCE/DOCKET NUMBER: 25585-A  
TELEPHONE: 816/474-9050  
TELEFAX: 816/474-9057  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-024-975-2

Query Match 100.0%; Score 96; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRRLPPRI 16  
| | | | | | | | | |  
Db 11 RPRPPPPPPRRLPPRI 26

RESULT 6  
US-08-930-777A-2  
Sequence 2, Application US/08930777A

Patent No. 6713605  
GENERAL INFORMATION:  
APPLICANT: Blecha, Frank  
APPLICANT: Shi, Jishu  
TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hovey, Williams, Timmons & Collins  
STREET: 2405 Grand Blvd., Ste. 400  
CITY: Kansas City  
STATE: Missouri  
COUNTRY: U.S.A.  
ZIP: 64108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,777A  
FILING DATE: October 8, 1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/04674  
FILING DATE: April 10, 1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26,262  
REFERENCE/DOCKET NUMBER: 23625-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-930-777A-2

Query Match 100.0%; Score 96; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRRLPPRI 16  
| | | | | | | | | |  
Db 11 RPRPPPPPPRRLPPRI 26

RESULT 7  
US-09-739-535-1  
Sequence 1, Application US/09739535  
Patent No. 679490  
GENERAL INFORMATION:  
APPLICANT: Cubist Pharmaceuticals, Inc.  
TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS  
FILE REFERENCE: C060  
CURRENT APPLICATION NUMBER: US/09/739,535  
CURRENT FILING DATE: 2000-12-15  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 38  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-739-535-1

Query Match 100.0%; Score 96; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 RPRPPPPPPRLPPRI 16  
Db 11 RPRPPPPPPRLPPRI 26

RESULT 8  
US-08-162-052-1  
; Sequence 1, Application US/08162052  
; Patent No. 5489575  
; GENERAL INFORMATION:  
; APPLICANT: LEE, Jong-Youn  
; APPLICANT: BOMAN, Hans G  
; APPLICANT: MUTT, Viktor  
; APPLICANT: JORNVAL, Hans  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/162,052  
; FILING DATE: 02-JUN-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9101838-2  
; FILING DATE: 14-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO 92-22578  
; FILING DATE: 23-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crane-Feury, Sharon E  
; REGISTRATION NUMBER: 36,113  
; REFERENCE/DOCKET NUMBER: 003300-299  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-162-052-1

Query Match 100.0%; Score 96; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRLPPRI 16  
Db 11 RPRPPPPPPRLPPRI 26

RESULT 9  
US-08-310-722-1  
; Sequence 1, Application US/08310722  
; Patent No. 5654273  
; GENERAL INFORMATION:  
; APPLICANT: Gallo, Richard L.  
; APPLICANT: Klagsbrun, Michael  
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair  
; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 1100 Peachtree Street, Suite 2800  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-4530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/310,722  
; FILING DATE: 22-SEP-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: CMCC379  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-815-6508  
; TELEFAX: (404)-815-6555  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; PUBLICATION INFORMATION:  
; AUTHORS: Lee, Jong-Youn  
; AUTHORS: Boman, Hans G.  
; AUTHORS: Mutt, Viktor  
; AUTHORS: Jornvall, Hans  
; TITLE: No. 5654273el Polypeptides And Their Use  
; JOURNAL: PCT WO 92/22578  
; DATE: 12/23/92  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39  
; US-08-310-722-1

Query Match 100.0%; Score 96; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPPPRLPPRI 16  
Db 11 RPRPPPPPPRLPPRI 26

RESULT 10  
US-08-419-066-1  
; Sequence 1, Application US/08419066  
; Patent No. 5830993  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &  
; ADDRESSEE: Collins  
; STREET: 2405 Grand Boulevard, Suite 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25



;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/419,066  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Collins, John M.  
;; REGISTRATION NUMBER: 26262  
;; REFERENCE/DOCKET NUMBER: 23625  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (816) 474-9050  
;; TELEFAX: (816) 474-9057  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 39 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
US-08-419-066-1

Query Match 100.0%; Score 96; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
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Db 11 RPRPPPPFPRLPPRI 26

RESULT 11  
US-08-728-333-1  
; Sequence 1, Application US/08728333  
; Patent No. 5863897  
; GENERAL INFORMATION:  
; APPLICANT: Gallo, Richard L.  
; APPLICANT: Klagsbrun, Michael  
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 1100 Peachtree Street, Suite 2800  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-4530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/728,333  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/310,722  
; FILING DATE: 22-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: CMCC379  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-815-6508  
; TELEFAX: (404)-815-6555  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; PUBLICATION INFORMATION:  
;; AUTHORS: Lee, Jong-Youn  
;; AUTHORS: Boman, Hans G.  
;; AUTHORS: Mutt, Viktor  
;; AUTHORS: Jornvall, Hans  
;; TITLE: No. 5863897el Polypeptides And Their Use  
;; JOURNAL: PCT WO 92/22578  
;; DATE: 12/23/92  
;; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39  
US-08-728-333-1

Query Match 100.0%; Score 96; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
|||  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 12  
US-09-024-975-1  
; Sequence 1, Application US/09024975  
; Patent No. 613233  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, CHRISTOPHER R.  
; APPLICANT: BLECHA, FRANK  
; APPLICANT: SHI, JISHU  
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
; STREET: 2405 GRAND BLVD., SUITE 400  
; CITY: KANSAS CITY  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/024,975  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/802,306  
; FILING DATE: 18-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COLLINS, JOHN M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 25585-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 816/474-9050  
; TELEFAX: 816/474-9057  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-024-975-1

Query Match 100.0%; Score 96; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
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Db 11 RPRPPPPFPRLPPRI 26

RESULT 13  
US-08-930-777A-1  
; Sequence 1, Application US/08930777A  
; Patent No. 6713605  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-930-777A-1

Query Match 100.0%; Score 96; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 14  
PCT-US95-12080-1  
; Sequence 1, Application PC/TUS9512080  
; GENERAL INFORMATION:  
; APPLICANT: Children's Medical Center Corporaton  
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/12080  
; FILING DATE:  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-873-8794  
; TELEFAX: (404)-815-8795  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; PUBLICATION INFORMATION:  
; AUTHORS: Lee, Jong-Youn  
; AUTHORS: Boman, Hans G.  
; AUTHORS: Mutt, Viktor  
; AUTHORS: Jornvall, Hans  
; TITLE: Novel Polypeptides And Their Use  
; JOURNAL: PCT WO 92/22578  
; DATE: 12/23/92  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39  
PCT-US95-12080-1

Query Match 100.0%; Score 96; DB 5; Length 39;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 15  
US-09-179-558-66  
; Sequence 66, Application US/09179558  
; Patent No. 6180612  
; GENERAL INFORMATION:  
; APPLICANT: Hockensmith, Joel W.  
; APPLICANT: Muthuswami, Rohini  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: TARGETING DNA METABOLIC PROCESSES USING  
; TITLE OF INVENTION: AMINOGLYCOSIDE DERIVATIVES  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/179,558  
; FILING DATE: 27-OCT-1998  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 09/060,470  
; FILING DATE: 15-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 60/063,898  
; FILING DATE: 31-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 9426-005-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-179-558-66

Query Match 65.6%; Score 63; DB 3; Length 311;  
Best Local Similarity 70.6%; Pred. No. 2.1;  
Matches 12; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

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Db 26 PPPPPFFPSLPPRLPP 42

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OM protein - protein search, using sw model

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Title: US-10-014-147-5

Perfect score: 96

Sequence: 1 RPRPPPPFPRLPPRI 16

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Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	96	100.0	16	15 US-10-651-147-5	Sequence 5, Appli
3	96	100.0	23	14 US-10-014-147-3	Sequence 3, Appli
4	96	100.0	23	15 US-10-651-147-3	Sequence 3, Appli
5	96	100.0	26	14 US-10-014-147-2	Sequence 2, Appli
6	96	100.0	26	15 US-10-651-147-2	Sequence 2, Appli
7	96	100.0	38	9 US-09-738-742-1	Sequence 1, Appli
8	96	100.0	38	9 US-09-739-535-1	Sequence 1, Appli
9	96	100.0	39	14 US-10-014-147-1	Sequence 1, Appli
10	96	100.0	39	15 US-10-391-155-1	Sequence 1, Appli
11	96	100.0	39	15 US-10-391-155-2	Sequence 2, Appli

12	96	100.0	39	15 US-10-391-155-6	Sequence 6, Appli
13	96	100.0	39	15 US-10-651-147-1	Sequence 1, Appli
14	96	100.0	42	16 US-10-344-709C-18	Sequence 18, Appli
15	96	100.0	42	17 US-10-916-185-14	Sequence 14, Appli
16	96	100.0	42	18 US-10-991-286A-44	Sequence 44, Appli
17	96	100.0	42	20 US-11-004-379-20	Sequence 20, Appli
18	75	78.1	304	14 US-10-156-761-13550	Sequence 13550, A
19	66	68.8	91	16 US-10-425-115-200180	Sequence 200180,
20	65	67.7	153	16 US-10-425-115-268716	Sequence 268716,
21	63	65.6	129	16 US-10-425-115-224656	Sequence 224656,
22	63	65.6	232	16 US-10-425-115-190616	Sequence 190616,
23	62	64.6	90	16 US-10-437-963-126573	Sequence 126573,
24	62	64.6	182	16 US-10-425-115-346674	Sequence 346674,
25	62	64.6	187	16 US-10-425-115-220493	Sequence 220493,
26	62	64.6	333	16 US-10-437-963-169542	Sequence 169542,
27	61	63.5	132	16 US-10-767-701-51171	Sequence 51171, A
28	61	63.5	209	16 US-10-425-115-207591	Sequence 207591,
29	61	63.5	256	16 US-10-437-963-128526	Sequence 128526,
30	61	63.5	266	16 US-10-425-115-189501	Sequence 189501,
31	61	63.5	322	16 US-10-425-115-316075	Sequence 316075,
32	60	62.5	191	16 US-10-425-115-285148	Sequence 285148,
33	60	62.5	204	16 US-10-437-963-180133	Sequence 180133,
34	60	62.5	425	16 US-10-437-963-108858	Sequence 108858,
35	60	62.5	431	16 US-10-437-963-204963	Sequence 204963,
36	60	62.5	520	9 US-09-726-643-102	Sequence 102, App
37	60	62.5	520	13 US-10-042-141-102	Sequence 102, App
38	60	62.5	520	17 US-10-919-272-102	Sequence 102, App
39	60	62.5	521	10 US-09-809-391-392	Sequence 392, App
40	60	62.5	521	10 US-09-882-171-392	Sequence 392, App
41	60	62.5	521	15 US-10-164-861-392	Sequence 392, App
42	60	62.5	526	9 US-09-925-300-1473	Sequence 1473, Ap
43	59.5	62.0	80	15 US-10-424-599-231660	Sequence 231660,
44	59	61.5	103	15 US-10-424-599-258982	Sequence 258982,
45	59	61.5	204	16 US-10-425-115-342021	Sequence 342021,

ALIGNMENTS

RESULT 1  
US-10-014-147-5  
; Sequence 5, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/014,147  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A



```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-014-147-5
Query Match 100.0%; Score 96; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16
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Db 1 RPRPPPPFPRLPPRI 16

RESULT 2
US-10-651-147-5
; Sequence 5, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/651,147
; FILING DATE: 28-Aug-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-651-147-5
Query Match 100.0%; Score 96; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16
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Db 1 RPRPPPPFPRLPPRI 16

RESULT 3
US-10-014-147-3
; Sequence 3, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-014-147-3
Query Match 100.0%; Score 96; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16
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Db 8 RPRPPPPFPRLPPRI 23

RESULT 4
US-10-651-147-3
; Sequence 3, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.

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Db 11 RRRPPPPFFPPRLPPRI 26  
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RESULT 7  
US-09-738-742-1  
; Sequence 1, Application US/09738742  
; Publication No. US2002025924A1  
; GENERAL INFORMATION:  
; APPLICANT: Cubist Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS  
; FILE REFERENCE: C060  
; CURRENT APPLICATION NUMBER: US/09/738,742  
; CURRENT FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-738-742-1  
Query Match 100.0%; Score 96; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPPPPFFPPRLPPRI 16  
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Db 11 RRRPPPPFFPPRLPPRI 26  
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RESULT 8  
US-09-739-535-1  
; Sequence 1, Application US/09739535  
; Publication No. US20020058785A1  
; GENERAL INFORMATION:  
; APPLICANT: Cubist Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS  
; FILE REFERENCE: C060  
; CURRENT APPLICATION NUMBER: US/09/739,535  
; CURRENT FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-739-535-1  
Query Match 100.0%; Score 96; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPPPPFFPPRLPPRI 16  
|||  
Db 11 RRRPPPPFFPPRLPPRI 26  
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RESULT 9  
US-10-014-147-1  
; Sequence 1, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins

; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/014,147  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-014-147-1  
Query Match 100.0%; Score 96; DB 14; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPPPPFFPPRLPPRI 16  
|||  
Db 11 RRRPPPPFFPPRLPPRI 26  
|||  
RESULT 10  
US-10-391-155-1  
; Sequence 1, Application US/10391155  
; Publication No. US20040009463A1  
; GENERAL INFORMATION:  
; APPLICANT: Simons, Michael  
; Gao, Youhe  
; TITLE OF INVENTION: Method for PR-39 peptide mediated  
; selective inhibition of IKBA degradation  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David Prashker, Esq.  
; STREET: P.O. Box 5387  
; CITY: Magnolia  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 01930  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
; COMPUTER: Dell PC  
; OPERATING SYSTEM: MS XP  
; SOFTWARE: WordPerfect version 10  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/391,155  
; FILING DATE: 18-Mar-2003  
; CLASSIFICATION: Unknown  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David Prashker, Esq.  
; REGISTRATION NUMBER: 29,693

REFERENCE/DOCKET NUMBER: BIS-044/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-391-155-1

Query Match 100.0%; Score 96; DB 15; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 11

US-10-391-155-2  
Sequence 2, Application US/10391155  
Publication No. US20040009463A1  
GENERAL INFORMATION:  
APPLICANT: Simons, Michael  
Gao, Youhe

TITLE OF INVENTION: Method for PR-39 peptide mediated  
selective inhibition of IKBA degradation

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:  
ADDRESSEE: David Prashker, Esq.  
STREET: P.O. Box 5387  
CITY: Magnolia  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 01930

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

COMPUTER: Dell PC  
OPERATING SYSTEM: MS XP  
SOFTWARE: WordPerfect version 10  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/391,155  
FILING DATE: 18-Mar-2003  
CLASSIFICATION: Unknown

ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker, Esq.  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: BIS-044/D

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-391-155-2

Query Match 100.0%; Score 96; DB 15; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 12

US-10-391-155-6  
Sequence 6, Application US/10391155  
Publication No. US20040009463A1  
GENERAL INFORMATION:  
APPLICANT: Simons, Michael  
Gao, Youhe

TITLE OF INVENTION: Method for PR-39 peptide mediated  
selective inhibition of IKBA degradation

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:  
ADDRESSEE: David Prashker, Esq.  
STREET: P.O. Box 5387  
CITY: Magnolia  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 01930

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
COMPUTER: Dell PC  
OPERATING SYSTEM: MS XP  
SOFTWARE: WordPerfect version 10  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/391,155  
FILING DATE: 18-Mar-2003  
CLASSIFICATION: Unknown

ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker, Esq.  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: BIS-044/D

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-391-155-6

Query Match 100.0%; Score 96; DB 15; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPRPPPPFPRLPPRI 16  
Db 11 RPRPPPPFPRLPPRI 26

RESULT 13

US-10-651-147-1  
Sequence 1, Application US/10651147  
Publication No. US20040043934A1  
GENERAL INFORMATION:  
APPLICANT: Blecha, Frank  
Shi, Jishu

TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hovey, Williams, Timmons & Collins  
STREET: 2405 Grand Blvd., Ste. 400  
CITY: Kansas City  
STATE: Missouri  
COUNTRY: U.S.A.  
ZIP: 64108

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/651,147  
; FILING DATE: 28-Aug-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-651-147-1

Query Match 100.0%; Score 96; DB 15; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRPFPFPFPPRLPPRI 16  
|||  
Db 11 RRPFPFPFPPRLPPRI 26

RESULT 14

US-10-344-709C-18  
; Sequence 18, Application US/10344709C  
; Publication No. US20040170642A1  
; GENERAL INFORMATION:

; APPLICANT: JORG FRITZ ET AL.  
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin  
; TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof  
; FILE REFERENCE: SONN:030US  
; CURRENT APPLICATION NUMBER: US/10/344,709C  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP01/09529  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: A 1416/2000  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-10-344-709C-18

Query Match 100.0%; Score 96; DB 16; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRPFPFPFPPRLPPRI 16  
|||  
Db 11 RRPFPFPFPPRLPPRI 26

RESULT 15

US-10-916-185-14  
; Sequence 14, Application US/10916185  
; Publication No. US20050107325A1  
; GENERAL INFORMATION:  
; APPLICANT: Manoharan, Muthiah

; APPLICANT: Kesavan, Venkitasamy  
; APPLICANT: Rajeev, Kallanthottathil G.  
; TITLE OF INVENTION: MODIFIED iRNA AGENTS  
; FILE REFERENCE: 14174-091001  
; CURRENT APPLICATION NUMBER: US/10/916,185  
; CURRENT FILING DATE: 2004-08-10  
; PRIOR APPLICATION NUMBER: PCT/US2004/011829  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 60/465,665  
; PRIOR FILING DATE: 2003-04-25  
; PRIOR APPLICATION NUMBER: US 60/463,772  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: US 60/469,612  
; PRIOR FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: US 60/465,802  
; PRIOR FILING DATE: 2003-04-25  
; PRIOR APPLICATION NUMBER: US 60/493,986  
; PRIOR FILING DATE: 2003-08-08  
; PRIOR APPLICATION NUMBER: US 60/494,597  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: US 60/503,414  
; PRIOR FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 60/506,341  
; PRIOR FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: US 60/510,246  
; PRIOR FILING DATE: 2003-10-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Exemplary Cell Permeation Peptides  
US-10-916-185-14

Query Match 100.0%; Score 96; DB 17; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRPFPFPFPPRLPPRI 16  
|||  
Db 11 RRPFPFPFPPRLPPRI 26

Search completed: October 26, 2005, 05:28:57  
Job time : 60.0545 secs



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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:51:43 ; Search time 59.0455 Seconds  
(without alignments)  
98.253 Million cell updates/sec

Title: US-10-014-147-6  
Perfect score: 92  
Sequence: 1 RPPGFPFPPFP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	92	100.0	15	2	AAW01449	Aaw01449	Leukocyte
2	92	100.0	15	8	ADE86117	Ade86117	Proline-a
3	92	100.0	15	8	ADL67259	Adl67259	Antimicro
4	92	100.0	39	2	AAR30491	Aar30491	Antibacte
5	92	100.0	39	2	AAR99121	Aar99121	Magainin-
6	92	100.0	39	2	AAR94446	Aar94446	Synducin
7	92	100.0	39	2	AAW01446	Aaw01446	Leukocyte
8	92	100.0	39	2	AAW75722	Aaw75722	Proline/A
9	92	100.0	39	3	AAB26888	Aab26888	PR-39 pep
10	92	100.0	39	4	AAB97280	Aab97280	PR-39 pep
11	92	100.0	39	4	AAB84690	Aab84690	Amino aci
12	92	100.0	39	8	ADD35364	Add35364	Antimicro
13	92	100.0	39	8	ADE86112	Ade86112	Proline-a
14	92	100.0	39	8	ADL67254	Adl67254	Antimicro
15	92	100.0	42	5	ABB07714	Abb07714	Antimicro
16	92	100.0	42	8	ADR82250	Adr82250	Cell perm
17	92	100.0	44	4	AAB51194	Aab51194	E. coli A
18	57.5	62.5	366	7	ADJ69455	Adj69455	Human hea
19	57	62.0	16	2	AAW01448	Aaw01448	Leukocyte
20	57	62.0	16	2	AAW75724	Aaw75724	Proline/A
21	57	62.0	16	8	ADE86116	Ade86116	Proline-a
22	57	62.0	16	8	ADL67258	Adl67258	Antimicro
23	57	62.0	23	2	AAW01451	Aaw01451	Leukocyte
24	57	62.0	23	8	ADE86114	Ade86114	Proline-a
25	57	62.0	23	8	ADL67256	Adl67256	Antimicro

26	57	62.0	26	2	AAW01447	Aaw01447	Leukocyte
27	57	62.0	26	2	AAW75723	Aaw75723	Proline/A
28	57	62.0	26	8	ADE86113	Ade86113	Proline-a
29	57	62.0	26	8	ADL67255	Adl67255	Antimicro
30	57	62.0	213	2	AAW05824	Aay05824	Arabidops
31	56	60.9	560	7	ADC38726	Adc38726	Human sec
32	56	60.9	741	7	ABO44410	Abo44410	Novel hum
33	56	60.9	769	7	ABO44402	Abo44402	Novel hum
34	56	60.9	801	7	ABO44394	Abo44394	Novel hum
35	56	60.9	829	7	ABO44386	Abo44386	Novel hum
36	56	60.9	894	7	ABO44407	Abo44407	Novel hum
37	56	60.9	922	7	ABO44399	Abo44399	Novel hum
38	56	60.9	954	7	ABO44391	Abo44391	Novel hum
39	56	60.9	982	7	ABO44383	Abo44383	Novel hum
40	56	60.9	1419	8	ADN03630	Adn03630	Antipsori
41	56	60.9	1981	8	ADS11120	Ads11120	Human the
42	56	60.9	2004	7	ABO44409	Abo44409	Novel hum
43	56	60.9	2032	7	ABO44401	Abo44401	Novel hum
44	56	60.9	2064	7	ABO44393	Abo44393	Novel hum
45	56	60.9	2092	7	ABO44385	Abo44385	Novel hum

ALIGNMENTS

RESULT 1  
AAW01449  
ID AAW01449 standard; peptide; 15 AA.  
XX  
AC AAW01449;  
XX  
DT 18-JUN-1997 (first entry)  
XX  
DE Leukocyte O2- production inhibitor peptide PR15.  
XX  
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;  
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;  
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;  
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;  
KW tissue damage; oxygen radical; inflammatory disease; therapy.  
XX  
OS Synthetic.  
XX  
PN WO9632129-A1.  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-US004674.  
XX  
PR 10-APR-1995; 95US-00419066.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 1996-476842/47.  
XX  
PT Inhibition of leukocyte super:oxide anion prodn. and attraction of  
leukocytes - using peptide(s) partic. based on antimicrobial PR-39.  
PS Claim 12; Page 28; 45pp; English.  
XX  
CC AAW01447-W01454 represent fragments of the proline-arginine rich  
antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first  
isolated from porcine small intestine, and has also been identified in  
human and porcine neutrophils. PR39 kills bacteria by interfering with  
DNA and/or protein synthesis. PR39 also induces syndecan expression on  
mesenchymal cells. Syndecans are important in wound repair, showing that  
PR39 can be used in wound repair, as well as in antibacterial agents.  
CC These sequences, and PR39, can be used in the method of the invention.  
CC The method of the invention is for inhibiting leukocyte superoxide anion  
(O2-) production. The method comprises administering to a leukocyte a  
peptide (such as this sequence) capable of inhibiting leukocyte O2-

CC production. The peptides can be used as medicaments for fighting  
CC infection by attracting leukocytes to a wound site and restricting tissue  
CC damage at the wound site caused by excessive oxygen radicals produced by  
CC these leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states  
XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 92; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIPPGFPPRFPFRFP 15  
| | | | | | | | | | | | | | |  
Db 1 RIPPGFPPRFPFRFP 15

RESULT 2  
ADE86117  
ID ADE86117 standard; peptide; 15 AA.  
XX  
AC ADE86117;

DT 29-JAN-2004 (first entry)  
XX  
DE Proline-arginine (PR)-rich antimicrobial peptide PR-15.  
XX

KW Leukocyte superoxide anion; leukocyte O2- production;  
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;  
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;  
KW tissue damage; oxygen radical; antibacterial.

OS Synthetic.  
XX  
XX US2003125249-A1.  
PN  
XX  
PD 03-JUL-2003.

XX  
PF 07-DEC-2001; 2001US-00014147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.

XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.

XX Blecha F, Shi J;  
DR WPI; 2004-059188/06.

XX Attracting leukocyte to location by administering peptide including  
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to  
PT the location.

XX Claim 3; SEQ ID NO 6; 24pp; English.

XX The present invention relates to a method of inhibiting leukocyte  
CC superoxide anion (O2-) production and/or attracting leukocytes. The  
CC method comprises the use of proline-arginine (PR)-rich antimicrobial  
CC peptides or their truncated analogues. The method is useful for  
CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or  
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are  
CC useful as medicaments to fight infection by attracting leukocytes to a  
CC wound site, while restricting tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leukocytes. The present  
CC sequence represents a PR-rich antimicrobial peptide.

XX Sequence 15 AA;

Query Match 100.0%; Score 92; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIPPGFPPRFPFRFP 15  
| | | | | | | | | | | | | | |  
Db 1 RIPPGFPPRFPFRFP 15  
RESULT 3  
ADL67259  
ID ADL67259 standard; peptide; 15 AA.  
XX  
AC ADL67259;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39 analog PR-15.  
XX

KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;  
KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;  
KW infection; wound; tissue damage; PR-39 analog; PR-15.

XX Unidentified.  
OS  
XX US2004043934-A1.  
PN  
XX 04-MAR-2004.

XX 28-AUG-2003; 2003US-00651147.

XX 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.

XX (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.

XX Blecha F, Shi J;  
PI  
XX WPI; 2004-225728/21.

XX Inhibiting leukocyte oxygen radical production comprises contacting a  
PT leukocyte with a peptide, where the inhibition occurs as a consequence of  
PT binding between the peptide and p47phox.

XX Example; SEQ ID NO 6; 24pp; English.

XX The invention relates to inhibiting leukocyte superoxide anion (O2-) production using a naturally occurring proline-arginine (PR)-rich antimicrobial peptide known as PR-39 and its truncated analogs. The method comprises contacting leukocytes with the peptide comprising 39 or 26 amino acids, for a time and under conditions effective to inhibit leukocyte superoxide anion production. The peptide inhibits the activity of NADPH oxidase responsible for anion production, by binding to Src homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or porcine leukocyte and the mammalian leukocyte is neutrophil. Another method is also disclosed which employs a PR-39 analog that comprise 16 amino acids, where the sum of the proline and arginine residues in the effective peptide is at least 66 or 74 % of the total number of amino acids. This peptide inhibits leukocyte O2- production by the effective binding to p47phox in whole cells, therefore interfering with the binding of p47phox to p22phox. At least 14 or 25% of the amino acid residues in the peptide are arginine residues. The method of the invention is useful for inhibiting leukocyte oxygen radical production. The peptides are useful as medicaments for fighting infections by attracting leukocytes to a wound site, yet restrict tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence is PR-39 analog, PR-15.

XX Sequence 15 AA;

Query Match 100.0%; Score 92; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIPPGFPPRFPFRFP 15

Db ||||||| 1 RPPGFPPRFP 15

RESULT 4

AAR30491

ID AAR30491 standard; peptide; 39 AA.

XX

AC AAR30491;

XX

DT 25-MAR-2003 (revised)

DT 12-MAY-1993 (first entry)

XX

DE Antibacterial peptide.

XX

KW Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;

KW veterinary medicine; prophylactic.

XX

OS Sus scrofa domestica.

XX

PN WO9222578-A1..

XX

PD 23-DEC-1992.

XX

PF 10-JUN-1992; 92WO-SE000394.

XX

PR 14-JUN-1991; 91SE-00001838.

XX

PA (LEEJ/) LEE J.

PA (BOMA/) BOMAN H G.

PA (MUTT/) MUTT V.

PA (JOER/) JOERNVALL H.

XX

PI Lee J, Boman HG, Mutt V, Joernvall H;

XX

DR WPI; 1993-018080/02.

XX

PT New anti-bacterial polypeptide - active against Gram negative bacteria.

XX

PS Claim 1; Page 10; 15pp; English.

XX

CC This peptide was isolated from the small intestine of a pig. The small intestine is an important endocrine organ and many physiologically active peptides have been isolated from it. This peptide inhibits the growth of, and may kill, bacteria, pref. gram negative bacteria. This peptide or its functional derivatives may be used in human or veterinary medicine for therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.00044;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPPGFPPRFP 15

Db 25 RPPGFPPRFP 39

RESULT 5

AAR99121

ID AAR99121 standard; peptide; 39 AA.

XX

AC AAR99121;

XX

DT 28-OCT-1996 (first entry)

XX

DE Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.

XX

KW STD; sexually transmitted disease; HIV; human immunodeficiency virus;

KW herpes simplex virus; HSV; Neisseria gonorrhoeae; Candida; Chlamydia;

KW magainin; antimicrobial; squalamine.

XX Synthetic.

OS

XX

FH Key

FT Modified-site 39

FT /note= "amidated"

XX

PN WO9608270-A2.

XX

PD 21-MAR-1996.

XX

PF 13-SEP-1995; 95WO-US011675.

XX

PR 13-SEP-1994; 94US-00305475.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Jacob L, Zasloff M, Williams T, Bedi G;

XX

DR WPI; 1996-179725/18.

XX

PT Inhibiting sexually transmitted disease e.g. HIV or herpes simplex - by administering magainin antimicrobial or squalamine cpd. to inhibit transmission.

PT

XX

PS Example 1; Page 32; 60pp; English.

XX

CC AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may be used to treat sexually transmitted diseases (STDs) caused by Chlamydia, HIV, herpes simplex virus, Neisseria gonorrhoeae or Candida infection.

CC

CC The peptides inhibit STDs by either killing the infectious organism,

CC impeding the infection mechanism or interrupting the replication cycle of the organism.

CC

CC fish shark Squalus acanthias) and PGLa (a frog antimicrobial peptide) analogues may also be useful in inhibiting STD infection and transmission

XX

SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 2; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.00044;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPPGFPPRFP 15

Db 25 RPPGFPPRFP 39

RESULT 6

AAR94446

ID AAR94446 standard; peptide; 39 AA.

XX

AC AAR94446;

XX

DT 05-NOV-1996 (first entry)

XX

DE Synducin peptide (PR-39) induces syndecan expression.

XX

KW Synducin; induction; expression; syndecan-1; syndecan-4; surface;

KW mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis;

KW decubitus; ulcers; keloids; skin burns; ischemic tissues;

KW hypercoagulation states; prevention; tumour metastasis; restenosis;

KW inhibition; angiogenesis; proliferation; endothelial.

XX

OS Synthetic.

XX

PN WO9609322-A2.

XX

PD 28-MAR-1996.

XX

PF 22-SEP-1995; 95WO-US012080.

XX

PR 22-SEP-1994; 94US-00310722.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.  
XX  
PI Gallo RL, Bernfield M;  
XX  
XX WPI; 1996-188401/19.  
DR  
XX  
PT Modulating mesenchymal interaction by administration of synducin - used  
PT in the treatment of wounds, tumours, restenosis, etc.  
PS  
XX Claim 4; Page 26; 34pp; English.  
XX  
CC The present peptide is a synducin, which induces the expression of  
CC syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.  
CC fibroblasts and epithelial cells. The 36 N-terminal amino acids of the  
CC peptide were found to be identical to the 36 N-terminal amino acids of PR  
CC -39, a Pro and Arg rich antibacterial peptide previously found in porcine  
CC intestine (WO9222578). Synducins may be used in the treatment of stasis  
CC and decubitus ulcers, keloids, skin burns, ischemic tissues and  
CC hypercoagulation states, prevention of tumour metastasis, restenosis  
CC inhibition and endothelial cell angiogenesis and proliferation induction.  
CC Human microvascular endothelial cells were assayed for syndecan-4  
CC expression following exposure to 5 % wound fluid, dbcAMP (1 mM), the  
CC present peptide (10 microM) or a blank, to give respective cell surface  
CC syndecan-4 values (mOD/m in) of approx. 1.75, 1.70, 1.80 and 0.95  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRFPFRFP 15  
| | | | | | | | | | | | | | |  
Db 25 RPPGFPFRFPFRFP 39

RESULT 7  
AAW01446  
ID AAW01446 standard; peptide; 39 AA.  
XX  
AC AAW01446;  
XX  
DT 18-JUN-1997 (first entry)  
XX  
DE Leukocyte O2- production inhibitor peptide PR39.  
XX  
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;  
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;  
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;  
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;  
KW tissue damage; oxygen radical; inflammatory disease; therapy.  
XX  
OS Synthetic.  
XX  
XX WO9632129-A1.  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-US004674.  
XX  
PR 10-APR-1995; 95US-00419066.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
XX Blecha F, Shi J;  
PI  
XX WPI; 1996-476842/47.  
DR  
XX Inhibition of leukocyte super:oxide anion prodn. and attraction of  
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.  
XX  
XX Claim 2; Page 26; 45pp; English.  
PS  
XX

CC This sequence represents the proline-arginine rich antimicrobial peptide  
CC PR39. The PR39 sequence was first isolated from porcine small intestine,  
CC and has also been identified in human and porcine neutrophils. PR39 kills  
CC bacteria by interfering with DNA and/or protein synthesis. PR39 also  
CC induces syndecan expression on mesenchymal cells. Syndecans are important  
CC in wound repair, showing that PR39 can be used in wound repair, as well  
CC as in antibacterial agents. This sequence, and the fragments of it shown  
CC in AAW01447-W01454, can be used in the method of the invention. The  
CC method of the invention is for inhibiting leukocyte superoxide anion (O2-  
CC ) production. The method comprises administering to a leukocyte a peptide  
CC (such as this sequence) capable of inhibiting leukocyte O2- production.  
CC The peptides can be used as medicaments for fighting infection by  
CC attracting leukocytes to a wound site and restricting tissue damage at  
CC the wound site caused by excessive oxygen radicals produced by these  
CC leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states

XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRFPFRFP 15  
| | | | | | | | | | | | | | |  
Db 25 RPPGFPFRFPFRFP 39

RESULT 8  
AAW75722  
ID AAW75722 standard; peptide; 39 AA.  
XX  
AC AAW75722;  
XX

DT 19-NOV-1998 (first entry)

XX Proline/Arginine rich peptide PR-39.

XX Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;  
KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;  
KW coronary bypass; organ transplantation surgery.  
XX

OS Synthetic.

XX WO9835690-A1.

XX 20-AUG-1998.

PF 17-FEB-1998; 98WO-US003207.

PR 18-FEB-1997; 97US-00802306.

PR 16-FEB-1998; 98US-00024975.

XX (UNIV ) UNIV KANSAS STATE RES FOUND.

XX Ross CR, Blecha F, Shi J;

XX WPI; 1998-495359/42.

XX Reduction of reperfusion injury in temporarily occluded blood vessels -  
PT by administration of a peptide which is rich in proline or arginine  
PT residues.

XX Claim 3; Page 14; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon  
CC administration into a mammal's bloodstream reduce reperfusion injury  
CC (production of reactive oxygen species, neutrophil adherence to  
CC endothelium, and extravasation of neutrophils). These peptides have two  
CC requirements: they contain the consensus sequence PXXP, where P is a  
CC proline residue and X is any amino acid residue, which has been found to  
CC inhibit superoxide production, and secondly they have arginine residues  
CC adjacent to these motifs, required for effective inhibition. It was



CC established by structural and function analysis that a peptide should  
CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is  
CC correlated with the increase of length of peptides. The effectiveness of  
CC these peptides was determined by investigating the production of the  
CC neutrophil superoxide anion, and also the inhibition of neutrophil  
CC chemotaxis. From this, it was found that all of the peptides inhibited  
CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil  
CC oxidase activity. PR-39 is believed, to be the most potent endogenous  
CC down regulator of NADPH oxidase yet discovered, and from the data  
CC produced, it can be suggested to be involved in eliminating or reducing  
CC the reperfusion injury induced adhesion and extraction of neutrophils.  
CC The peptides are also useful in connection with surgical procedures such  
CC as coronary bypass and organ transplantation surgery  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRFPFRFP 15  
Db 25 RPPGFPFRFPFRFP 39  
|||||

RESULT 9  
AAB26888  
ID AAB26888 standard; peptide; 39 AA.

XX AAB26888;

DT 01-FEB-2001 (first entry)

DE PR-39 peptide used in angiogenesis control.

XX Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;  
KW myocardial ischaemia; proteasome.

XX Synthetic.

XX WO200057895-A1.

PN 05-OCT-2000.

PD 16-MAR-2000; 2000WO-US007050.

XX 26-MAR-1999; 99US-00276868.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Simons M, Gao Y;

XX WPI; 2000-628319/60.

XX Stimulating angiogenesis in situ, useful e.g. for treating anoxia and  
PT infarction, by administering a PR-39 oligopeptide that regulates  
PT enzymatic activity of proteasomes.

XX Disclosure; Page 21; 51pp; English.

XX This invention relates to a method for the stimulation of angiogenesis in  
CC situ within a targeted collection of viable cells. The method comprises  
CC introducing, into the cytoplasm, at least i member of the PR-39  
CC oligopeptide collective, which interacts with cytoplasmic proteasomes.  
CC Part of the proteolytic activity of the proteasomes is selectively  
CC altered so as to stimulate angiogenesis. The method is used to induce  
CC angiogenesis in tissue that has suffered anoxia or infarction, e.g.  
CC myocardial infarction or chronic myocardial ischaemia, and also to study  
CC the mechanisms that control angiogenesis. The present sequence represents  
CC the PR-39 peptide from which peptide used in the method of the invention  
CC are derived  
XX

SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRFPFRFP 15  
Db 25 RPPGFPFRFPFRFP 39  
|||||

RESULT 10

AAB97280  
ID AAB97280 standard; peptide; 39 AA.

XX AAB97280;

DT 09-AUG-2001 (first entry)

DE PR-39 peptide.

XX PR-39; cathelin; inflammation; wound healing; myocardial infarction;  
KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;  
KW anoxia; chronic myocardial ischaemia; heart tissue.

XX Unidentified.

XX WO200130368-A1.

XX 03-MAY-2001.

XX 06-OCT-2000; 2000WO-US027552.

PF 25-OCT-1999; 99US-00426011.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Simons M, Gao Y;

XX WPI; 2001-355179/37.

XX Stimulation of angiogenesis and inhibition of proteasome mediated  
PT degradation in cells, by introduction of PR-39 oligopeptide or its N-  
PT terminal fragments or their conjugates, for use in anoxia and infarction  
PT conditions.

XX Disclosure; Page 21; 52pp; English.

XX Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39  
CC is a member of the the cathelin family of proteins, mature PR-39  
CC represented by the present sequence is 39 amino acids in length, and has  
CC been shown to play a role in several inflammatory events including wound  
CC healing and myocardial infarction. The PR-39 derived family of  
CC oligopeptides cause selective inhibition of proteasome mediated  
CC degeneration of peptides and stimulation of angiogenesis after their  
CC intracellular introduction to a target cell. PR-39 derived peptides are  
CC able to interact with at least the alpha7 subunit of the proteasomes, and  
CC therefore alter the proteolytic activity of proteasomes such that a  
CC selective increased expression of specific proteins occurs. The invention  
CC includes methods for the selective inhibition of proteasome mediated  
CC peptide degradation. The method provides means for stimulating  
CC angiogenesis as required in living tissues and organs which have suffered  
CC defects or have undergone anoxia and/or infarction, myocardial infarction  
CC or chronic myocardial ischaemia of heart tissue. Examples are the  
CC myocardium, skeletal or smooth muscle, artery or vein, lung, brain,  
CC kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and  
CC extremities. A particular example is after myocardial infarction or  
CC ischaemia

XX Sequence 39 AA;

Query Match 100.0%; Score 92; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 RIPPGFPPRFPFRFP 15  
Db 25 RIPPGFPPRFPFRFP 39

RESULT 11  
AAB84690  
ID AAB84690 standard; protein; 39 AA.  
XX  
AC AAB84690;  
XX  
DT 17-SEP-2001 (first entry)  
DE Amino acid sequence of a PR-39 protein.  
XX  
KW PR-39; IkappaBalpa degradation; NFkappaB transcription factor;  
KW myocardial infarction; chronic myocardial ischemia; heart disease;  
KW anoxia.  
XX  
OS Unidentified.  
XX  
PN WO200147540-A1.  
XX  
PD 05-JUL-2001.  
XX  
PF 27-DEC-2000; 2000WO-US035293.  
XX  
PR 29-DEC-1999; 99US-00474967.  
XX  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Simons M, Gao Y;  
XX  
DR WPI; 2001-441690/47.  
XX  
PT Selective inhibition of IkappaBalpa degradation within targeted viable  
PT cell collection, involves interacting PR-39 oligopeptide with  
PT IkappaBalpa and proteasomes, and altering proteolytic activity of  
PT proteasomes.  
XX  
PS Disclosure; Page 30; 69pp; English.  
XX

CC The present sequence represents a PR-39 protein. The specification  
CC describes PR-39 derived peptides, which are used for selective inhibition  
CC of IkappaBalpa degradation within a targeted cell collection in-situ.  
CC The method is useful for selectively inhibiting IkappaBalpa protein  
CC degradation in situ, decreasing the activity of NFkappaB transcription  
CC factor and selective control of NFkappaB-dependent gene expression in  
CC situ. The PR-39 derived peptides are useful in the treatment of  
CC myocardial infarction, chronic myocardial ischemia of heart disease and  
CC anoxia  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIPPGFPPRFPFRFP 15  
Db 25 RIPPGFPPRFPFRFP 39

RESULT 12  
ADD35364  
ID ADD35364 standard; peptide; 39 AA.  
XX  
AC ADD35364;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39.

XX antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological;  
KW intraocular pressure; glaucoma; ocular hypertension; hyperaemia;  
KW irritation; inflammation; conjunctiva; ocular cell dysplasia;  
KW iridial melanocyte hyperplasia; hyperpigmentation.  
XX  
OS Unidentified.  
XX  
PN WO2003079997-A2.  
XX  
PD 02-OCT-2003.  
XX  
PF 21-MAR-2003; 2003WO-US008935.  
XX  
PR 21-MAR-2002; 2002US-0367071P.  
XX  
PA (CAYM-) CAYMAN CHEM CO.  
XX  
PI Maxey KM, Johnson J;  
XX  
DR WPI; 2004-011506/01.  
XX  
PT Ophthalmic solution useful for the treatment of increased intraocular  
PT pressure comprises a prostaglandin of the F-series and an antimicrobial  
PT peptide.  
XX  
PS Disclosure; Page 11; 11pp; English.  
XX

CC The invention relates to a novel ophthalmic solution comprising a  
CC prostaglandin of the F-series and an antimicrobial peptide. A solution of  
CC the invention has hypotensive and ophthalmological activity. The solution  
CC is useful for the treatment of increased intraocular pressure, such as  
CC caused by glaucoma and for the reduction of ocular hypertension. The  
CC prostaglandin and the antimicrobial peptide work synergistically, to  
CC provide beneficial reduction in the incidence of irritant and toxic side  
CC effects such as hyperaemia, irritation and inflammation of conjunctiva,  
CC ocular cell dysplasia, iridial melanocyte hyperplasia, and  
CC hyperpigmentation, associated with the prior art prostaglandin  
CC compositions. The present sequence represents an antimicrobial peptide of  
CC the invention.  
XX  
SQ Sequence 39 AA;

Query Match 100.0%; Score 92; DB 8; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIPPGFPPRFPFRFP 15  
Db 25 RIPPGFPPRFPFRFP 39

RESULT 13  
ADE86112  
ID ADE86112 standard; peptide; 39 AA.  
XX  
AC ADE86112;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Proline-arginine (PR)-rich antimicrobial peptide PR-39.  
XX  
KW Leukocyte superoxide anion; leukocyte O2- production;  
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;  
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;  
KW tissue damage; oxygen radical; antibacterial.  
XX  
OS Synthetic.  
XX  
PN US2003125249-A1.  
XX  
PD 03-JUL-2003.  
XX

PF 07-DEC-2001; 2001US-00014147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 2004-059188/06.  
XX  
XX Attracting leukocyte to location by administering peptide including  
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to  
PT the location.  
XX  
PS Claim 2; SEQ ID NO 1; 24pp; English.  
XX  
CC The present invention relates to a method of inhibiting leukocyte  
CC superoxide anion (O2-) production and/or attracting leukocytes. The  
CC method comprises the use of proline-arginine (PR)-rich antimicrobial  
CC peptides or their truncated analogues. The method is useful for  
CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or  
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are  
CC useful as medicaments to fight infection by attracting leukocytes to a  
CC wound site, while restricting tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leukocytes. The present  
CC sequence represents a PR-rich antimicrobial peptide.  
XX  
SQ Sequence 39 AA;  
  
Query Match 100.0%; Score 92; DB 8; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RIPPGFPPRFPFRFP 15  
Db |||||  
25 RIPPGFPPRFPFRFP 39  
  
RESULT 14  
ADL67254  
ID ADL67254 standard; peptide; 39 AA.  
XX  
AC ADL67254;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39.  
XX  
KW Leucocyte ; superoxide anion; oxygen radical; proline-arginine ;  
KW antimicrobial; antioxidant; NADPH oxidase ; p47phox; neutrophil;  
KW infection; wound ; tissue damage ; PR-39 peptide.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .26  
FT /label= PR-26\_peptide  
FT Peptide 1. .19  
FT /label= PR-19\_peptide  
FT Peptide 1. .14  
FT /label= PR-14\_peptide  
FT Region 1. .3  
FT /note= "Essential for antibacterial activity"  
FT Peptide 4. .26  
FT /label= PR-23\_peptide  
FT Peptide 11. .26  
FT /label= PR-16\_peptide  
FT Region 20. .26  
FT /note= "Essential for antibacterial activity"  
FT Peptide 25. .39  
FT /label= PR-15\_peptide

XX US2004043934-A1.  
PN  
XX  
PD 04-MAR-2004.  
XX  
PF 28-AUG-2003; 2003US-00651147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 2004-225728/21.  
XX  
PT Inhibiting leukocyte oxygen radical production comprises contacting a  
PT leukocyte with a peptide, where the inhibition occurs as a consequence of  
PT binding between the peptide and p47phox.  
XX  
PS Claim 1; SEQ ID NO 1; 24pp; English.  
XX  
CC The invention relates to inhibiting leukocyte superoxide anion (O2-) production using a naturally occurring proline-arginine (PR)-rich antimicrobial peptide known as PR-39 and its truncated analogs. The method comprises contacting leukocytes with the peptide comprising 39 or 26 amino acids, for a time and under conditions effective to inhibit leukocyte superoxide anion production. The peptide inhibits the activity of NADPH oxidase responsible for anion production, by binding to Src homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or porcine leukocyte and the mammalian leukocyte is neutrophil. Another method is also disclosed which employs a PR-39 analog that comprise 16 amino acids, where the sum of the proline and arginine residues in the effective peptide is at least 66 or 74 % of the total number of amino acids. This peptide inhibits leukocyte O2- production by the effective binding to p47phox in whole cells, therefore interfering with the binding of p47phox to p22phox. At least 14 or 25% of the amino acid residues in the peptide are arginine residues. The method of the invention is useful for inhibiting leukocyte oxygen radical production. The peptides are useful as medicaments for fighting infections by attracting leukocytes to a wound site, yet restrict tissue damage at the wound site caused by excessive oxygen radicals produced by these leukocytes. The present sequence is PR-39 peptide.  
XX  
SQ Sequence 39 AA;  
  
Query Match 100.0%; Score 92; DB 8; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RIPPGFPPRFPFRFP 15  
Db |||||  
25 RIPPGFPPRFPFRFP 39  
  
RESULT 15  
ABB07714  
ID ABB07714 standard; peptide; 42 AA.  
XX  
AC ABB07714;  
XX  
DT 10-JUN-2002 (first entry)  
XX  
DE Antimicrobial peptide PR-39 C-terminal fragment.  
XX  
KW Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;  
KW antigen presenting cell; adjuvant; porcine; PR-39.  
XX  
OS Sus sp.  
XX  
PN WO200213857-A2.

XX 21-FEB-2002.  
PD  
XX  
XX PF 17-AUG-2001; 2001WO-EP009529.  
XX  
XX PR 17-AUG-2000; 2000AT-00001416.  
XX  
XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
XX  
XX PI Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;  
XX WFI; 2002-269154/31.  
DR  
XX  
XX Vaccine for active immunization or for preparing an adjuvant for  
PT enhancing an immune response to at least one antigen, comprises at least  
PT one antigen and at least one cathelicidin derived antimicrobial peptide.  
XX  
XX Disclosure; Fig 3; 65pp; English.  
PS  
XX The invention relates to a vaccine comprising at least one antigen and at  
CC least one cathelicidin derived antimicrobial peptide or its derivative.  
CC The vaccine is useful for active immunization, especially of humans or  
CC animals without protection against the specific antigen. The cathelicidin  
CC derived antimicrobial peptide is useful in the preparation of an adjuvant  
CC for enhancing the immune response to at least one antigen, where the  
CC adjuvant enhances the uptake of at least one antigen in antigen  
CC presenting cells (APC), and the adjuvant is added to the vaccine.  
CC Sequences ABB07708-15 represent C-terminal fragments of antimicrobial  
CC peptides of the cathelicidin family  
XX  
SQ Sequence 42 AA;

Query Match 100.0%; Score 92; DB 5; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.00047;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPPRPFRFP 15  
| | | | | | | | | | | | | | | |  
Db 25 RPPGFPPRPFRFP 39

Search completed: October 26, 2005, 05:12:08  
Job time : 60.0455 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 11.1818 Seconds  
(without alignments)  
129.071 Million cell updates/sec

Title: US-10-014-147-6  
Perfect score: 92  
Sequence: 1 RPPGFPFRPPRP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	92	100.0	172	2 S68232	antimicrobial prot
2	57	62.0	213	2 T48490	embryo-specific pr
3	55	59.8	866	1 JC4305	dynamin II - human
4	54	58.7	428	2 T48008	hypothetical prote
5	53.5	58.2	212	2 S57330	cathelin-like anti
6	53.5	58.2	228	2 S40463	prophenin (PR-2) p
7	53	57.6	741	2 T00206	epidermis-specific
8	53	57.6	1029	2 T30351	mucin-like protein
9	52.5	57.1	1560	2 T42727	proliferation pote
10	52	56.5	134	2 D84672	hypothetical prote
11	52	56.5	388	2 JC5437	spliceosome-associ
12	51.5	56.0	948	2 A57640	retinoblastoma bin
13	51	55.4	743	1 S23779	collagen alpha 1(V
14	51	55.4	744	1 A34246	collagen alpha 1(V
15	51	55.4	744	1 S23298	collagen alpha 1(V
16	51	55.4	744	2 S15435	collagen alpha 1(V
17	51	55.4	868	2 A36878	dynamin 2 - rat
18	51	55.4	870	2 B53165	dynamin II isoform
19	51	55.4	870	2 A53165	dynamin II isoform
20	51	55.4	879	2 D96804	unknown protein T5
21	50	54.3	513	2 T37180	probable membrane
22	49	53.3	424	2 A54964	spliceosome-associ
23	48.5	52.7	147	2 A29149	proline-rich prote
24	48.5	52.7	164	2 A30496	proline-rich prote
25	48.5	52.7	172	2 B29149	proline-rich prote
26	48.5	52.7	204	2 A39066	proline-rich prote
27	48.5	52.7	223	2 A42817	proline-rich prote
28	48.5	52.7	564	2 H70804	hypothetical prote
29	48	52.2	199	2 S14981	extensin class I (

30	48	52.2	233	2 T32500	hypothetical prote
31	48	52.2	318	2 JE0284	Mm-1 cell derived
32	48	52.2	322	2 S09779	hypothetical prote
33	48	52.2	994	2 S19595	chloride channel p
34	47.5	51.6	218	2 A40513	hypothetical prote
35	47.5	51.6	230	2 T01561	hypothetical prote
36	47	51.1	191	2 D72711	hypothetical prote
37	47	51.1	319	2 T05584	hypothetical prote
38	47	51.1	485	2 S64945	probable membrane
39	47	51.1	554	2 T02445	probable U4/U6 sma
40	47	51.1	587	2 JC5669	Ca2+/calmodulin-de
41	47	51.1	609	2 T52524	hypothetical prote
42	47	51.1	997	2 S44457	period clock prote
43	47	51.1	1357	2 T29265	hypothetical prote
44	46.5	50.5	259	2 S74287	hypothetical prote
45	46.5	50.5	1026	1 A40315	maternal effect pr

ALIGNMENTS

RESULT 1

S68232  
antimicrobial protein PR-39 precursor, cathelin-associated - pig  
N;Alternate names: myeloid antibacterial protein PR-39  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S68232; JN0899; I47138; S19563  
R;Zhao, C.; Ganz, T.; Lehrer, R.I.  
FEBS Lett. 376, 130-134, 1995  
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni  
A;Reference number: S68232; MUID:96105365; PMID:7498526  
A;Accession: S68232  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-172 <ZHA>  
A;Cross-references: UNIPROT:P80054; EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g116:  
A;Experimental source: leukocytes  
R;Storici, P.; Zanetti, M.  
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993  
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i  
A;Reference number: JN0899; MUID:94071853; PMID:8250863  
A;Accession: JN0899  
A;Molecule type: mRNA  
A;Residues: 1-20,'A',22-172 <STO>  
A;Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101  
A;Experimental source: bone marrow cells  
R;Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bome  
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995  
A;Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami  
A;Reference number: I47138; MUID:95350216; PMID:7624374  
A;Accession: I47138  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-28,'T',30-89,'QR',92-116,'NDP',120-172 <GUD>  
A;Cross-references: EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PID:g1051298  
R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,  
Eur. J. Biochem. 202, 849-854, 1991  
A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of th  
A;Reference number: S19563; MUID:92111534; PMID:1765098  
A;Accession: S19563  
A;Molecule type: protein  
A;Residues: 131-169 <AGE>  
A;Experimental source: intestine  
C;Genetics:  
A;Gene: PR39  
A;Introns: 66/3; 102/3; 126/3  
C;Superfamily: cathelin; cystatin homology  
C;Keywords: amidated carboxyl end; antibacterial  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;22-129/Domain: cystatin homology <CYS>  
F;30-130/Domain: propeptide #status predicted <PRO>  
F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>



F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 100.0%; Score 92; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRFPFRFP 15  
|||||  
Db 155 RPPGFPFRFPFRFP 169  
|||||

RESULT 2  
T48490  
embryo-specific protein 3 (ATS3) - Arabidopsis thaliana  
N;Alternate names: protein T28J14.130  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48490  
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le  
submitted to the Protein Sequence Database, April 2000  
A;Reference number: Z24493  
A;Accession: T48490  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-213 <BEV>  
A;Cross-references: UNIPROT:Q9LYP6; EMBL:AL163652  
A;Experimental source: cultivar Columbia; BAC clone T28J14  
C;Genetics:  
A;Map position: 5  
A;Introns: 28/3; 65/3  
A;Note: T28J14.130

Query Match 62.0%; Score 57; DB 2; Length 213;  
Best Local Similarity 69.2%; Pred. No. 1.3;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPGFPFRFPFRFP 15  
|||  
Db 161 PPFPFPFPETP 173  
|||

RESULT 3  
JC4305  
dynamin II - human  
N;Alternate names: microtubule-binding protein  
C;Species: Homo sapiens (man)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 19-Jan-2001  
C;Accession: JC4305  
R;Diatloff-Zito, C.; Gordon, A.J.E.; Duchaud, E.; Merlin, G.  
Gene 163, 301-306, 1995  
A;Title: Isolation of an ubiquitously expressed cDNA encoding human dynamin II, a member  
A;Reference number: JC4305; MUID:96011652; PMID:7590285  
A;Accession: JC4305  
A;Molecule type: mRNA  
A;Residues: 1-866 <DIA>  
A;Cross-references: GB:L36983  
C;Comment: This protein is a cytoskeletal protein that functions in endocytosis and syna  
C;Genetics:  
A;Gene: GDB:DNM2  
A;Cross-references: GDB:696233  
A;Map position: 9q12-9q12  
C;Superfamily: human dynamin II; pleckstrin repeat homology  
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop; phosphoprotei  
F;38-45/Region: nucleotide-binding motif A (P-loop)  
F;132-137/Region: nucleotide-binding motif B  
F;508-620/Domain: protein kinase C substrate #status predicted <PKC>  
F;514-619/Domain: pleckstrin repeat homology <PLK>  
F;740-866/Region: proline-rich  
F;116,126,760/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicte  
F;175,274,323,404,742,762/Binding site: phosphate (Thr) (covalent) (by cdc2 kinase) #sta

Query Match 59.8%; Score 55; DB 1; Length 866;  
Best Local Similarity 66.7%; Pred. No. 9.7;

Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 RPPGFPFRFPFRFP 15  
|||||  
Db 833 RPPGIPPGVPSRRP 847  
|||||

RESULT 4  
T48008  
hypothetical protein T17J13.120 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48008  
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, F  
submitted to the Protein Sequence Database, February 2000  
A;Reference number: Z24482  
A;Accession: T48008  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-428 <RIE>  
A;Cross-references: UNIPROT:Q9M1Q8; EMBL:AL138651  
A;Experimental source: cultivar Columbia; BAC clone T17J13  
C;Genetics:  
A;Map position: 3  
A;Introns: 137/3  
A;Note: T17J13.120

Query Match 58.7%; Score 54; DB 2; Length 428;  
Best Local Similarity 64.3%; Pred. No. 6.3;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IPPGFPFRFPFRFP 15  
|||  
Db 200 ISPAIPFPFPAPFP 213  
|||

RESULT 5  
S57330  
cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)  
N;Alternate names: antimicrobial peptide; prophenin-1  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S57330; S68726  
R;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V.  
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995  
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte  
A;Reference number: S57330; MUID:96042752; PMID:7576250  
A;Accession: S57330  
A;Molecule type: mRNA  
A;Residues: 1-212 <STR>  
A;Cross-references: UNIPROT:P51524; GB:X86031; NID:g1006756; PIDN:CAA60023.1; PID:g100675  
R;Harwig, S.S.L.; Kokryakov, V.N.; Swiderek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer, R.I.  
FEBS Lett. 362, 65-69, 1995  
A;Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcine le  
A;Reference number: S68726; MUID:95212585; PMID:7698355  
A;Accession: S68726  
A;Molecule type: protein  
A;Residues: 131-209 <HAR>  
A;Experimental source: leukocytes  
C;Superfamily: cathelin; cystatin homology  
C;Keywords: antibacterial  
F;6-113/Domain: cystatin homology <CYS>

Query Match 58.2%; Score 53.5; DB 2; Length 212;  
Best Local Similarity 60.0%; Pred. No. 3.6;  
Matches 12; Conservative 0; Mismatches 1; Indels 7; Gaps 2;

QY 3 PPGFP-PRFP-----PRFP 15  
|||  
Db 144 PPNFPGFRFPFPFPFP 163  
|||

RESULT 6



```

RESULT 8
T30351
mucin-like protein - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30351
R/Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrer,
Virology 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30351
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1029 <KUZ>
A:Cross-references: UNIPROT:Q9YMX0; EMBL:AF081810; PIDN:AAC70189.1

Query Match 57.6%; Score 53; DB 2; Length 1029;
Best Local Similarity 80.0%; Pred. NO. 21;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PGGFPPRFP 12
||| |||: |||
Db 938 PPFPFPQFP 947

RESULT 9
T42727
proliferation potential-related protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42727
R/Witte, M.M.; Scott, R.E.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z22246
A:Accession: T42727
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1560 <WIT>
A:Cross-references: UNIPROT:P97868; EMBL:U83913; NID:g3858884; PID:g3858885; PIDN:AAC7243
A:Experimental source: strain Balb/c
C:Genetics:
A:Gene: P2P-R
A:Function:
A:Description: involved in hnRNP association and Rb1 binding
F:57-107/Domain: RING finger homology <RRN>

Query Match 57.1%; Score 52.5; DB 2; Length 1560;
Best Local Similarity 60.0%; Pred. NO. 37;
Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 2 IPPGFPPRFP 15
: ||| |||: |||
Db 376 LPPGVLPFPQFSPQFP 390

RESULT 10
D84672
hypothetical protein At2g27390 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: D84672
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84672
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <STO>

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A;Cross-references: UNIPROT:Q9XIP3; GB:AE002093; NID:g5306259; PIDN:AAD41991.1; GSPDB:GN	
C;Genetics:	
A;Gene: At2g27390	
A;Map position: 2	
Query Match 56.5%; Score 52; DB 2; Length 134;	
Best Local Similarity 60.0%; Pred. No. 3.5;	
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;	
QY 1 RPPGFPPRPFRFP 15	
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Db 54 RLPPFPFALFPFPFP 68	
RESULT 11	
JC5437	
spliceosome-associated protein 49 - Caenorhabditis elegans	
C;Species: Caenorhabditis elegans	
C;Date: 17-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 16-Aug-2004	
C;Accession: JC5437	
R;Tanaka, Y.; Ohta, A.; Terashima, K.; Sakamoto, H.	
J. Biochem. 121, 739-745, 1997	
A;Title: Polycistronic expression and RNA-binding specificity of the C. elegans homolog	
A;Reference number: JC5437; MUID:97306058; PMID:9163526	
A;Accession: JC5437	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-388 <TAN>	
A;Cross-references: UNIPROT:Q17352; GB:U24189	
C;Comment: This protein is a subunit of splicing factor SF3b and is involved in U2 small	
C;Superfamily: ribonucleoprotein repeat homology	
F;14-97,101-184/Region: RNA recognition pattern	
F;14-81/Domain: ribonucleoprotein repeat homology <RRM4>	
F;101-169/Domain: ribonucleoprotein repeat homology <RRM2>	
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Db 342 RYPGMPFPFPFRYP 356	
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C;Species: Homo sapiens (man)	
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004	
C;Accession: A57640	
R;Sakai, Y.; Saijo, M.; Coelho, K.; Kishino, T.; Niikawa, N.; Taya, Y.	
Genomics 30, 98-101, 1995	
A;Title: cDNA sequence and chromosomal localization of a novel human protein, RBQ-1 (RB	
A;Reference number: A57640; MUID:96129310; PMID:8595913	
A;Accession: A57640	
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-948 <SAK>	
A;Cross-references: UNIPROT:Q15290; GB:X85133; NID:g728590; PIDN:CAA59445.1; PID:g755748	
C;Genetics:	
A;Gene: GDB:RBBP6	
A;Cross-references: GDB:626076	
A;Map position: 16p12-16p11.2	
C;Keywords: tandem repeat; zinc	
F;79-129/Domain: RING finger homology <RNG>	
Query Match 56.0%; Score 51.5; DB 2; Length 948;	
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Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;	
QY 2 IPPGF-PPRFPFRFP 15	
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Db 398 LPPGVPPPPQFSPQFP 412	
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collagen alpha 1(VIII) chain - mouse	
C;Species: Mus musculus (house mouse)	
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004	
C;Accession: S23779	
R;Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Ninomiya, Y.	
Eur. J. Biochem. 207, 895-902, 1992	
A;Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polypeptic	
A;Reference number: S23779; MUID:92362626; PMID:1499564	
A;Accession: S23779	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-743 <MUR>	
A;Cross-references: UNIPROT:Q00780; EMBL:X66976; NID:g50493; PIDN:CAA47387.1; PID:g13599;	
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology	
F;616-742/Domain: complement Clq carboxyl-terminal homology <ClQ>	
Query Match 55.4%; Score 51; DB 1; Length 743;	
Best Local Similarity 50.0%; Pred. No. 27;	
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QY 2 IPPGFPPRPFRFP 15	
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Db 36 LPPQIPPPQIPPPQIP 49	
RESULT 14	
A34246	
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C;Species: Oryctolagus cuniculus (domestic rabbit)	
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004	
C;Accession: A34246	
R;Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Ninomiya, Y.	
J. Biol. Chem. 264, 16022-16029, 1989	
A;Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that type	
omains similar to those of type X collagen.	
A;Reference number: A34246; MUID:89380199; PMID:2476437	
A;Accession: A34246	
A;Molecule type: mRNA	
A;Residues: 1-744 <YAM>	
A;Cross-references: UNIPROT:P14282; GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896	
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology	
F;1-20/Domain: signal sequence #status predicted <SIG>	
F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>	
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F;118-571/Region: interrupted helical	
F;572-744/Region: carboxyl-terminal nonhelical	
F;617-743/Domain: complement Clq carboxyl-terminal homology <ClQ>	
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Best Local Similarity 50.0%; Pred. No. 27;	
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QY 2 IPPGFPPRPFRFP 15	
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Db 36 LPPQIPPPQIPPPQIP 49	
RESULT 15	
S23298	
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C;Species: Gallus gallus (chicken)	
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004	
C;Accession: S23298	
R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McCa	
maguchi, N.; Olsen, B.R.	
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pres	
A;Title: The molecular biology of collagens with short triple-helical domains.	
A;Reference number: S22243	

A;Accession: S23298  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-744 <NIN>  
A;Cross-references: UNIPROT:Q7LZR2  
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology  
F;617-743/Domain: complement Clq carboxyl-terminal homology <ClQ>

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Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPPGFPPRPPRFP 15  
Db 36 LPPQIPPQMPQP 49

Search completed: October 26, 2005, 05:20:01  
Job time : 13.1818 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:52:03 ; Search time 51.9545 Seconds  
(without alignments)  
147.844 Million cell updates/sec

Title: US-10-014-147-6  
Perfect score: 92  
Sequence: 1 RIPPGFPPRPFPFP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	92	100.0	172	1	PR39_PIG	P80054 sus scrofa
2	67	72.8	484	2	Q8ILQ0	Q8ilq0 plasmodium
3	63	68.5	415	2	Q7RQAO	Q7rqao plasmodium
4	57	62.0	213	2	Q81271	Q81271 arabidopsis
5	57	62.0	213	2	Q94K23	Q94k23 arabidopsis
6	57	62.0	213	2	Q9LYP6	Q9lyp6 arabidopsis
7	56	60.9	135	2	O61134	O61134 dictyosteli
8	56	60.9	139	2	O61135	O61135 dictyosteli
9	56	60.9	150	2	Q67VV4	Q67vv4 oryza sativ
10	56	60.9	150	2	Q6Z4P0	Q6z4p0 oryza sativ
11	56	60.9	2382	1	WNK1_HUMAN	Q9h4a3 homo sapien
12	55	59.8	393	2	Q9UPH5	Q9uph5 homo sapien
13	55	59.8	464	2	Q8N1K8	Q8nlk8 homo sapien
14	55	59.8	870	1	DYN2_HUMAN	P50570 homo sapien
15	54.5	59.2	213	2	Q7SHV3	Q7shv3 neurospora
16	54	58.7	428	2	Q9MLQ8	Q9mlq8 arabidopsis
17	54	58.7	480	2	Q740X0	Q740x0 mycobacteri
18	54	58.7	532	2	O61133	O61133 dictyosteli
19	54	58.7	851	2	Q7ZUE4	Q7zue4 brachydanio
20	54	58.7	910	2	Q6FNO8	Q6fn08 candida gla
21	53.5	58.2	212	1	PF11_PIG	P51524 sus scrofa
22	53.5	58.2	228	1	PF12_PIG	P51525 sus scrofa
23	53.5	58.2	902	2	Q9DBK8	Q9dbk8 mus musculu
24	53.5	58.2	941	2	Q91W60	Q91w60 mus musculu
25	53.5	58.2	941	2	Q8C7K5	Q8c7k5 mus musculu
26	53.5	58.2	942	2	O54882	O54882 mus musculu
27	53.5	58.2	942	2	Q8C7G9	Q8c7g9 mus musculu
28	53	57.6	121	2	Q6ZH25	Q6zh25 oryza sativ
29	53	57.6	454	2	Q91Z39	Q91z39 mus musculu
30	53	57.6	548	2	Q6ESK7	Q6esk7 oryza sativ
31	53	57.6	552	2	O76861	O76861 drosophila

32	53	57.6	741	2	O15999	O15999 ciona savig
33	53	57.6	1029	2	Q9YMX0	Q9ymx0 lymantria d
34	52.5	57.1	678	2	Q653U4	Q653u4 oryza sativ
35	52	56.5	134	2	Q9XIP3	Q9xip3 arabidopsis
36	52	56.5	195	2	Q62WB3	Q6zwb3 homo sapien
37	52	56.5	236	2	Q657Y0	Q657y0 oryza sativ
38	52	56.5	388	2	Q8T8N6	Q8t8n6 caenorhabdi
39	52	56.5	398	2	Q17352	Q17352 caenorhabdi
40	52	56.5	541	2	Q7RYV7	Q7ryv7 neurospora
41	52	56.5	788	2	Q6PI09	Q6pi09 homo sapien
42	52	56.5	858	2	Q8NCZ1	Q8ncz1 homo sapien
43	52	56.5	871	2	Q6NWC9	Q6nwy9 homo sapien
44	52	56.5	873	2	Q9WVC9	Q9wvc9 mus musculu
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ALIGNMENTS

RESULT 1  
PR39\_PIG  
ID PR39\_PIG STANDARD; PRT; 172 AA.  
AC P80054; Q9TR84;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antibacterial protein PR-39 precursor.  
GN Name=PR39;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95350216; PubMed=7624374;  
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,  
RA Andersson L., Boman H.G.;  
RT "Structure of the gene for porcine peptide antibiotic PR-39, a  
RT cathelin gene family member: comparative mapping of the locus for the  
RT human peptide antibiotic FALL-39.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=94071853; PubMed=8250863;  
RA Storici P., Zanetti M.;  
RT "A cDNA derived from pig bone marrow cells predicts a sequence  
RT identical to the intestinal antibacterial peptide PR-39.";  
RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;  
RA Zhao C., Ganz T., Lehrer R.I.;  
RT "Structures of genes for two cathelin-associated antimicrobial  
RT peptides: prophenin-2 and PR-39.";  
RL FEBS Lett. 376:130-134(1995).  
RN [4]  
RP SEQUENCE OF 131-169.  
RC TISSUE=Intestine;  
RX MEDLINE=92111534; PubMed=1765098;  
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,  
RA Mutt V., Joernvall H.;  
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new  
RT member of the family of proline-arginine-rich antibacterial  
RT peptides.";  
RL Eur. J. Biochem. 202:849-854(1991).  
RN [5]  
RP SEQUENCE OF 131-164, AND FUNCTION.  
RC TISSUE=Neutrophils;  
RX MEDLINE=95088504; PubMed=7996056;  
RA Shi J., Ross C.R., Chengappa M.M., Blecha P.;  
RT "Identification of a proline-arginine-rich antibacterial peptide from



RT neutrophils that is analogous to PR-39, an antibacterial peptide from  
RT the small intestine.";  
RL J. Leukoc. Biol. 56:807-811(1994).  
CC -I- FUNCTION: Exerts a potent antimicrobial activity against both  
CC E.coli and B.megaterium.  
CC -I- TISSUE SPECIFICITY: Small intestine and bone marrow.  
CC -I- SIMILARITY: Belongs to the cathelicidin family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; X87236; CAA60682.1; -.  
DR EMBL; L23825; AAA31109.1; -.  
DR EMBL; X89201; CAA61487.1; -.  
DR PIR; S68232; S68232.  
DR HSSP; P32196; 1KWI.  
DR InterPro; IPR001894; Cathelicidin.  
DR Pfam; PF00666; Cathelicidins; 1.  
DR ProDom; PD001838; Cathelicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
KW Amidation; Antibiotic; Direct protein sequencing;  
KW Pyrrolidone carboxylic acid; Signal.  
FT SIGNAL 1 29 Potential.  
FT PROPEP 30 130  
FT CHAIN 131 169 Antibacterial protein PR-39.  
FT MOD\_RES 30 30 Pyrrolidone carboxylic acid (By  
FT similarity).  
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FT DISULFID 107 124 By similarity.  
FT MOD\_RES 169 169 Proline amide (G-170 provides amide  
FT group).  
FT CONFLICT 21 21 G -> A (in Ref. 2).  
FT CONFLICT 29 29 A -> T (in Ref. 1).  
FT CONFLICT 90 91 RQ -> QR (in Ref. 1).  
FT CONFLICT 117 119 IHS -> NDP (in Ref. 1).  
FT CONFLICT 157 157 P -> I (in Ref. 5).  
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Query Match 100.0%; Score 92; DB 1; Length 172;  
Best Local Similarity 100.0%; Pred. No. 0.0003;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RPPGFPPRPFRFP 15  
Db 155 RPPGFPPRPFRFP 169  
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Q8ILQ0  
ID Q8ILQ0 PRELIMINARY; PRT; 484 AA.  
AC Q8ILQ0;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)  
DE Spliceosome-associated protein, putative.  
GN ORFNames=PF14\_0194;  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;  
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,  
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,  
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,  
RA Chan M.S., Nene V., Shalloom S.J., Suh B., Peterson J., Angiuoli S.,  
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,  
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,  
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
RA Fraser C.M., Barrell B.;  
RT "Genome sequence of the human malaria parasite Plasmodium  
RT falciparum.";  
RL Nature 419:498-511(2002).  
DR EMBL; AE014819; AAN36806.1; -.  
DR HSSP; P11940; 1CVJ.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; RRM\_1; 2.  
DR SMART; SM00360; RRM; 2.  
DR PROSITE; PS50102; RRM; 2.  
SQ SEQUENCE 484 AA; 53722 MW; 0858953D48F72E2B CRC64;  
  
Query Match 72.8%; Score 67; DB 2; Length 484;  
Best Local Similarity 76.9%; Pred. No. 1.3;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 3 PPGFPPRPFRFP 15  
Db 429 PPGFPPNLPNFP 441  
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ID Q7RQA0 PRELIMINARY; PRT; 415 AA.  
AC Q7RQA0;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Splicing factor 3b subunit 4.  
GN Name=PY01202;  
OS Plasmodium yoelii yoelii.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=73239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=17XNL;  
RX PubMed=12368865; DOI=10.1038/nature01099;  
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,  
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
RA Shalloom S.J., van Aken S.E., Riedmuller S.B., Feldlyum T.V.,  
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,  
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
RA Carucci D.J.;  
RT "Genome sequence and comparative analysis of the model rodent malaria  
RT parasite Plasmodium yoelii yoelii.";  
RL Nature 419:512-519(2002).  
CC -I- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AABL01000316; EAA20492.1; -.  
DR HSSP; P11940; 1CVJ.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; RRM\_1; 2.  
DR PROSITE; PS50102; RRM; 2.  
SQ SEQUENCE 415 AA; 46441 MW; 6D9D28AF80357B0A CRC64;  
  
Query Match 68.5%; Score 63; DB 2; Length 415;  
Best Local Similarity 76.9%; Pred. No. 3.4;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 3 PPGFPPRPFRFP 15  
Db 350 PPGFPPFPFTFP 362  
|||||  
RESULT 4

SEQUENCE FROM N.A.  
Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,  
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
Ecker J., Theologis A., Davis R.W.;  
Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
EMBL: AF370461; AAK43838.1; -;  
EMBL: AY064694; AAL47396.1; -;  
InterPro: IPR010417; AT33.

GN name=pops;  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WS576;  
RX MEDLINE=98367519; PubMed=9692967; DOI=10.1021/bi9808013;  
RA Zhang Y., Brown R.D. Jr., West C.M.;

RT "Two proteins of the Dictyostelium spore coat bind to cellulose in vitro."  
RL Biochemistry 37:10766-10779(1998).  
DR EMBL; AF066072; AAC19124.1; -.  
DR DictyBase; DDB0185060; pspB.  
FT NON\_TER 1  
FT NON\_TER 135  
SQ SEQUENCE 135 AA; 14829 MW; 500634A988AA9408 CRC64;

Query Match 60.9%; Score 56; DB 2; Length 135;  
Best Local Similarity 53.8%; Pred. No. 7.7;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPGFPPRFPFRFP 15  
||:||||:|  
Db 38 PPSYPPSYPTYP 50

RESULT 8  
O61135 PRELIMINARY; PRT; 139 AA.  
AC O61135;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE SP85 (Fragment).  
GN Name=pspB;  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WS380B;  
RX MEDLINE=98367519; PubMed=9692967; DOI=10.1021/bi9808013;  
RA Zhang Y., Brown R.D. Jr., West C.M.;  
RT "Two proteins of the Dictyostelium spore coat bind to cellulose in vitro."  
RL Biochemistry 37:10766-10779(1998).  
DR EMBL; AF066073; AAC19125.1; -.  
DR DictyBase; DDB0185060; pspB.  
FT NON\_TER 1  
FT NON\_TER 139  
SQ SEQUENCE 139 AA; 15368 MW; 4862D2F15137553F CRC64;

Query Match 60.9%; Score 56; DB 2; Length 139;  
Best Local Similarity 53.8%; Pred. No. 8;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPGFPPRFPFRFP 15  
||:||||:|  
Db 38 PPSYPPSYPTYP 50

RESULT 9  
Q67VV4 PRELIMINARY; PRT; 150 AA.  
AC Q67VV4;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein OSJNBa0023122.10 (Hypothetical protein P0530H05.25).  
DE P0530H05.25).  
GN Name=OSJNBa0023122.10; Synonyms=P0530H05.25;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC clone:OSJNBa0023122.";

QY 3 PPGFPPRFPFRFP 15  
||:||||:|  
Db 38 PPSYPPSYPTYP 50

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC clone:P0530H05.";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP004733; BAD37715.1; -.  
DR EMBL; AP003541; BAD37390.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 150 AA; 16041 MW; 2C1B2FB6B092D311 CRC64;

Query Match 60.9%; Score 56; DB 2; Length 150;  
Best Local Similarity 66.7%; Pred. No. 8.7;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIPPGEPPRFPFRFP 15  
|:|||||  
Db 62 RLPPGLPFRPPARPP 76

RESULT 10  
Q6Z4P0 PRELIMINARY; PRT; 150 AA.  
AC Q6Z4P0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein OSJNBa0060017.6.  
GN Name=OSJNBa0060017.6;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC clone:OSJNBa0060017.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP005167; BAC83800.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 150 AA; 15983 MW; 31ADE779971F0350 CRC64;

Query Match 60.9%; Score 56; DB 2; Length 150;  
Best Local Similarity 66.7%; Pred. No. 8.7;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIPPGEPPRFPFRFP 15  
|:|||||  
Db 62 RLPPGLPFRPPARPP 76

RESULT 11  
WNK1 HUMAN STANDARD; PRT; 2382 AA.  
ID \_WNK1\_HUMAN  
AC Q9H4A3; O15052; Q86WL5; Q8N673; Q9P1S9;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Serine/threonine-protein kinase WNK1 (EC 2.7.1.37) (Protein kinase with no lysine 1) (Protein kinase, lysine-deficient 1) (Kinase deficient protein).  
DE with no lysine 1) (Protein kinase, lysine-deficient 1) (Kinase deficient protein).  
GN Name=PRKWNK1; Synonyms=KDP, KIAA0344;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND CHROMOSOMAL LOCATION.  
RC TISSUE=Heart;

QY 1 RIPPGEPPRFPFRFP 15  
|:|||||  
Db 62 RLPPGLPFRPPARPP 76



RX MEDLINE=21455683; PubMed=11571656; DOI=10.1038/sj/onc/1204726;  
RA Verlesimo F., Jordan P.;  
RT "WNK kinases, a novel protein kinase subfamily in multi-cellular  
RT organisms.";  
RL Oncogene 20:5562-5569(2001).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).  
RC TISSUE=Kidney;  
RX PubMed=14645531; DOI=10.1128/MCB.23.24.9208-9221.2003;  
RA Delaloy C., Lu J., Houot A.M., Disse-Nicodeme S., Gasc J.M.,  
RA Corvol P., Jeunemaitre X.;  
RT "Multiple promoters in the WNK1 gene: one controls expression of a  
RT kidney-specific kinase-defective isoform.";  
RL Mol. Cell. Biol. 23:9208-9221(2003).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Placenta;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP SEQUENCE OF 1-670 FROM N.A. (ISOFORM 1/2), FUNCTION, SUBCELLULAR  
RC LOCATION, AND TISSUE SPECIFICITY.  
RX TISSUE=Breast carcinoma;  
RL MEDLINE=20127920; PubMed=10660600; DOI=10.1074/jbc.275.6.4311;  
RA Moore T.M., Garg R., Johnson C., Coptcoat M.J., Ridley A.J.,  
RA Morris J.D.H.;  
RT "PSK, a novel STE20-like kinase derived from prostatic carcinoma that  
RT activates the JNK MAPK pathway and regulates actin cytoskeletal  
RT organisation.";  
RL J. Biol. Chem. 275:4311-4322(2000).  
RN [5]  
RP SEQUENCE OF 69-2382 FROM N.A. (ISOFORM 2).  
RC TISSUE=Brain;  
RX MEDLINE=97349984; PubMed=9205841;  
RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. VII.  
RT The complete sequences of 100 new cDNA clones from brain which can  
RT code for large proteins in vitro.";  
RL DNA Res. 4:141-150(1997).  
RN [6]  
RP REVISIONS TO N-TERMINUS.  
RX MEDLINE=22158633; PubMed=12168954;  
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
RT "Construction of expression-ready cDNA clones for KIAA genes: manual  
RT curation of 330 KIAA cDNA clones.";  
RL DNA Res. 9:99-106(2002).  
RN [7]  
RP DISEASE.  
RX MEDLINE=21390047; PubMed=11498583; DOI=10.1126/science.1062844;  
RA Wilson F.H., Disse-Nicodeme S., Choate K.A., Ishikawa K.,  
RA Nelson-Williams C., Desitter I., Gunel M., Milford D.V., Lipkin G.W.,  
RA Achard J.M., Feely M.P., Dussol B., Berland Y., Unwin R.J., Mayan H.,  
RA Simon D.B., Farfel Z., Jeunemaitre X., Lifton R.P.;

RT "Human hypertension caused by mutations in WNK kinases.";  
RL Science 293:1107-1112(2001).  
CC -!- FUNCTION: Controls sodium and chloride ion transport by inhibiting  
CC the activity of PRKWNK4, potentially by either phosphorylating the  
CC kinase or via an interaction between PRKWNK4 and the  
CC autoinhibitory domain of PRKWNK1. PRKWNK4 regulates the activity  
CC of the thiazide-sensitive Na-Cl cotransporter, SLC12A3, by  
CC phosphorylation. PRKWNK1 may also play a role in actin  
CC cytoskeletal reorganization.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- COFACTOR: Magnesium.  
CC -!- ENZYME REGULATION: By hypertonicity. Activation requires  
CC autophosphorylation of Ser-382. Phosphorylation of Ser-378 also  
CC promotes increased activity (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative promoter;  
CC Comment=2 isoforms, 1 (shown here) and 4, are produced by use of  
CC alternative promoters;  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1;  
CC IsoId=Q9H4A3-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9H4A3-2; Sequence=VSP\_050638;  
CC Note=No experimental confirmation available;  
CC Name=3;  
CC IsoId=Q9H4A3-3; Sequence=VSP\_050635, VSP\_050636;  
CC Name=4; Synonyms=Kidney-specific, Kinase-defective;  
CC IsoId=Q9H4A3-4; Sequence=VSP\_050634, VSP\_050637;  
CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels observed  
CC in the testis, heart, kidney and skeletal muscle.  
CC -!- DISEASE: Defects in PRKWNK1 are a cause of pseudohypoadosteronism  
CC type II (PHAII) [MIM:145260]. PHAII is an autosomal dominant  
CC disease characterized by severe hypertension, hyperkalemia, and  
CC sensitivity to thiazide diuretics which may result from a chloride  
CC shunt in the renal distal nephron.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. WNK  
CC subfamily.  
CC -!- CAUTION: Cys-250 is present instead of the conserved Lys which is  
CC expected to be an active site residue. Lys-233 appears to fulfill  
CC the required catalytic function.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AJ296290; CAC15059.1; -;  
CC EMBL; AY231477; AAO46160.1; -;  
CC EMBL; BC021121; AAH21121.1; -;  
CC EMBL; AF061944; AAF31483.1; -;  
CC EMBL; AB002342; BAA20802.2; -;  
CC Genew; HGNC:14540; PRKWNK1.  
CC MIM; 605232; -;  
CC MIM; 145260; -;  
CC GO; GO:0005737; C:cytoplasm; IDA.  
CC GO; GO:0005524; F:ATP binding; IDA.  
CC GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.  
CC GO; GO:0006811; P:ion transport; ISS.  
CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.  
CC GO; GO:0007243; P:protein kinase cascade; IDA.  
CC GO; GO:0050794; P:regulation of cellular process; ISS.  
CC InterPro; IPR011009; Kinase like.  
CC InterPro; IPR000719; Prot\_kinase.  
CC InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
CC Pfam; PF00069; Pkinase; 1.  
CC ProDom; PD000001; Prot\_kinase; 1.  
CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
CC PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
CC -----

KW Alternative promoter usage; Alternative splicing; ATP-binding;  
KW Phosphorylation; Protein kinase inhibitor;  
KW Serine/threonine-protein kinase; Transferase.  
FT DOMAIN 221 479 Protein kinase.  
FT NP\_BIND 227 235 ATP (By similarity).  
FT BINDING 233 233 ATP (By similarity).  
FT ACT\_SITE 349 349 Proton acceptor (By similarity).  
FT MOD\_RES 378 378 Phosphoserine (by autocatalysis) (By  
FT similarity).  
FT MOD\_RES 382 382 Phosphoserine (by autocatalysis) (By  
FT similarity).  
FT VARSPLIC 1 407 Missing (in isoform 4).  
FT VARSPLIC 386 393 TPEFMAPE -> MFQVYLGA (in isoform 3).  
FT VARSPLIC 394 2382 /FTID=VSP 050635.  
FT VARSPLIC 408 437 /FTID=VSP 050636.  
FT FGMCMLEMATSEYPYSECQNAAQIVRRVTS -> MDIKKKD  
FT FCSVFVIINSHCCCCCPQKDCINE (in isoform 4).  
FT /FTID=VSP 050637.  
FT VARSPLIC 792 1037 Missing (in isoform 2).  
FT /FTID=VSP 050638.  
FT CONFLICT 669 670 VS -> GG (in Ref. 4).  
FT CONFLICT 740 740 Missing (in Ref. 5).  
FT CONFLICT 1808 1808 I -> M (in Ref. 5).  
FT CONFLICT 1836 1836 Missing (in Ref. 5).  
SQ SEQUENCE 2382 AA; 250755 MW; ADDA6C86554B7FCA CRC64;

Query Match 60.9%; Score 56; DB 1; Length 2382;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GPPPRFPFRFP 15  
||||| ||:|  
Db 945 GPPRLPPQYP 955

RESULT 12

Q9UPH5 Q9UPH5 PRELIMINARY; PRT; 393 AA.  
AC Q9UPH5  
Q9UPH5  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Dynamin II (AA 474-866] (Fragment).  
GN Name=DNM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J.E., McCready P.M., Skowronski E., Richardson P.,  
RA Burkhardt-Schultz K., Gordon L., Dias J., Sakalsasis G., Stilwagen S.,  
RA Phan H., Velasco N., Do L., Regala W., Terry A., Scott D.,  
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J.,  
RA Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,  
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,  
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
RA Olsen A.S., Carrano A.V.;  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Contains 1 PH domain.  
DR EMBL; AC007229; AAD23603.1; -.  
DR HSSP; Q05193; 1DYN.  
DR GO; GO:0005525; F:GTP binding; IEA.  
DR GO; GO:0003924; F:GTPase activity; IEA.  
DR InterPro; IPR000375; Dynamin\_central.  
DR InterPro; IPR003130; GED.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR011036; PH related.  
DR Pfam; PF01031; Dynamin\_M; 1.  
DR Pfam; PF02212; GED; 1.  
DR Pfam; PF00169; PH; 1.

DR SMART; SM00302; GED; 1.  
DR SMART; SM00233; PH; 1.  
DR PROSITE; PS50003; PH\_DOMAIN; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 393 AA; 44036 MW; FAA7B8456023E2D1 CRC64;  
Query Match 59.8%; Score 55; DB 2; Length 393;  
Best Local Similarity 66.7%; Pred. No. 32;  
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 RIPPGFPPRFPFRFP 15  
||||| ||:|  
Db 360 RIPPGIPPGVPSRRP 374  
RESULT 13  
Q8N1K8 Q8N1K8 PRELIMINARY; PRT; 464 AA.  
AC Q8N1K8  
Q8N1K8  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein FLJ40556.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Thymus;  
RX PubMed=14702039; DOI=10.1038/ngi1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,  
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,  
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,  
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,  
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Okamoto S.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Senba T.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45(2004).  
CC -!- SIMILARITY: Contains 1 PH domain.  
DR EMBL; AK097875; BAC05190.1; -.  
DR HSSP; Q05193; 2DYN.  
DR GO; GO:0005525; F:GTP binding; IEA.  
DR GO; GO:0003924; F:GTPase activity; IEA.  
DR InterPro; IPR000375; Dynamin\_central.  
DR InterPro; IPR003130; GED.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR011036; PH related.  
DR Pfam; PF01031; Dynamin\_M; 1.  
DR Pfam; PF02212; GED; 1.  
DR Pfam; PF02212; GED; 1.



DR Pfam; PF00169; PH; 1.  
DR SMART; SM00302; GED; 1.  
DR SMART; SM00233; PH; 1.  
DR PROSITE; PS50003; PH\_DOMAIN; 1.  
SQ SEQUENCE 464 AA; 52198 MW; A56592DDAD9B7368 CRC64;  
  
Query Match 59.8%; Score 55; DB 2; Length 464;  
Best Local Similarity 66.7%; Pred. No. 39;  
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 RIPPFGPPRPFRFP 15  
Db 431 RIPPGIPPGVPSRRP 445  
  
RESULT 14  
DYN2\_HUMAN  
ID DYN2\_HUMAN STANDARD; PRT; 870 AA.  
AC P50570; Q725S3; Q9UPH4;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Dynamin 2 (EC 3.6.5.5).  
GN Name=DNM2; Synonyms=DYN2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RX MEDLINE=96011652; PubMed=7590285; DOI=10.1016/0378-1119(95)00275-B;  
RA Diatloff-Zito C., Gordon A.J.E., Duchaud E., Merlin G.;  
RT "Isolation of an ubiquitously expressed cDNA encoding human dynamin  
II, a member of the large GTP-binding protein family.";  
RL Gene 163:301-306(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX PubMed=15057824; DOI=10.1038/nature02399;  
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,  
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,  
RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,  
RA Caenepeel S., Carrano A.V., Caiole C., Chan Y.M., Christensen M.,  
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,  
RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,  
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,  
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,  
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,  
RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,  
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,  
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,  
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,  
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,  
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,  
RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,  
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,  
RA Rubin E.M., Lucas S.M.;  
RT "The DNA sequence and biology of human chromosome 19.";  
RL Nature 428:529-535(2004).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Uterus;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP INTERACTION WITH SHANK PROTEINS.  
RX MEDLINE=21611185; PubMed=11583995; DOI=10.1074/jbc.M104927200;  
RA Okamoto P.M., Gamby C., Wells D., Fallon J., Vallee R.B.;  
RT "Dynamin isoform-specific interaction with the shank/PROSAP  
scaffolding proteins of the postsynaptic density and actin  
cytoskeleton.";  
RL J. Biol. Chem. 276:48458-48465(2001).  
CC -!- FUNCTION: Microtubule-associated force-producing protein involved  
in producing microtubule bundles and able to bind and hydrolyze  
GTP. Most probably involved in vesicular trafficking processes, in  
particular endocytosis.  
CC -!- CATALYTIC ACTIVITY: GTP + H(2)O = GDP + phosphate.  
CC -!- SUBUNIT: Interacts with SHANK1 and SHANK2.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Microtubule-associated. Also  
found in the postsynaptic density of neuronal cells.  
CC -!- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Name=1;  
IsoId=P50570-1; Sequence=Displayed;  
Name=2;  
IsoId=P50570-2; Sequence=VSP\_001325;  
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed.  
CC -!- SIMILARITY: Belongs to the dynamin family.  
CC -!- SIMILARITY: Contains 1 PH domain.  
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL; L36983; AAA88025.1; --  
CC EMBL; AC007229; AAD23604.1; --  
CC EMBL; BC054501; AAH54501.1; --  
CC HSSP; Q05193; 2DYN.  
CC IntAct; P50570; --  
CC Genew; HGNC:2974; DNM2.  
CC MIM; 602378; --  
CC GO; GO:0000086; P:G2/M transition of mitotic cell cycle; TAS.  
CC InterPro; IPR001401; Dynamin.  
CC InterPro; IPR000375; Dynamin\_central.  
CC InterPro; IPR003130; GED.  
CC InterPro; IPR001849; PH.  
CC Pfam; PF01031; Dynamin\_M; 1.  
CC Pfam; PF00350; Dynamin\_N; 1.  
CC Pfam; PF02212; GED; 1.  
CC Pfam; PF00169; PH; 1.  
CC PRINTS; PR00195; DYNAMIN.  
CC SMART; SM00053; DYNC; 1.  
CC SMART; SM00302; GED; 1.  
CC SMART; SM00233; PH; 1.  
CC PROSITE; PS00410; DYNAMIN; 1.  
CC PROSITE; PS50003; PH\_DOMAIN; 1.  
KW Alternative splicing; Endocytosis; GTP-binding; Hydrolase;  
Microtubule; Motor protein; Multigene family.  
FT NP\_BIND 38 45 GTP (By similarity).  
FT NP\_BIND 136 140 GTP (By similarity).  
FT NP\_BIND 205 208 GTP (By similarity).  
FT DOMAIN 519 625 PH.  
FT VARSPLIC 516 519 Missing (in isoform 2).  
/FTid=VSP\_001325.

Job time : 53.9545 secs

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FT CONFLICT 316 316 N -> I (in Ref. 1).
FT CONFLICT 324 324 R -> P (in Ref. 1).
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Query Match 59.8%; Score 55; DB 1; Length 870;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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AC Q7SHV3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU02508.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryzstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000002; EAA36403.1; -.
DR HSSP; P14678; 1D3B.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
DR GO; GO:0008248; F:pre-mRNA splicing factor activity; IEA.
DR GO; GO:0006397; P:mRNA processing; IEA.
DR InterPro; IPR010920; Sm like_riboprot.
DR InterPro; IPR006649; snRNP.
DR InterPro; IPR001163; snRNP_Sm.
DR Pfam; PF01423; LSM; 1.
DR ProDom; PD020287; snRNP; 1.
KW Hypothetical protein.
SQ SEQUENCE 213 AA; 21440 MW; 17356AF1B36F2240 CRC64;
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Best Local Similarity 45.8%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 2; Indels 11; Gaps 1;

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Db 174 PPGFPVFPAPAGFCAGFPFPSP 197
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 15.4091 Seconds  
(without alignments)  
72.667 Million cell updates/sec

Title: US-10-014-147-6  
Perfect score: 92  
Sequence: 1 RIPPFGPPRPFRFP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	92	100.0	15	4 US-08-930-777A-6	Sequence 6, Appli
2	92	100.0	39	1 US-08-162-052-1	Sequence 1, Appli
3	92	100.0	39	1 US-08-310-722-1	Sequence 1, Appli
4	92	100.0	39	2 US-08-419-066-1	Sequence 1, Appli
5	92	100.0	39	2 US-08-728-333-1	Sequence 1, Appli
6	92	100.0	39	3 US-09-024-975-1	Sequence 1, Appli
7	92	100.0	39	4 US-08-930-777A-1	Sequence 1, Appli
8	92	100.0	39	5 PCT-US95-12080-1	Sequence 1, Appli
9	75.5	82.1	38	4 US-09-739-535-1	Sequence 1, Appli
10	57.5	62.5	78	1 US-08-487-359-5	Sequence 5, Appli
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19	56	60.9	769	4 US-09-854-856-44	Sequence 44, Appli
20	56	60.9	801	4 US-09-854-856-28	Sequence 28, Appli
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37	56	60.9	2245	4 US-09-854-856-4	Sequence 4, Appli
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44	53.5	58.2	79	1 US-08-487-359-1	Sequence 1, Appli
45	53.5	58.2	79	1 US-08-487-359-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-930-777A-6  
; Sequence 6, Application US/08930777A  
; Patent No. 6713605  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-930-777A-6

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Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RIPPFGPPRPFRFP 15  
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Db 1 RPPGFPPRFPFRFP 15

RESULT 2

US-08-162-052-1

; Sequence 1, Application US/08162052

; Patent No. 5489575

; GENERAL INFORMATION:

; APPLICANT: LEE, Jong-Youn

; APPLICANT: BOMAN, Hans G

; APPLICANT: MUTT, Viktor

; APPLICANT: JORNVAL, Hans

; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/162,052

; FILING DATE: 02-JUN-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9101838-2

; FILING DATE: 14-JUN-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO 92-22578

; FILING DATE: 23-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Crane-Feury, Sharon E

; REGISTRATION NUMBER: 36,113

; REFERENCE/DOCKET NUMBER: 003300-299

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-162-052-1

Query Match 100.0%; Score 92; DB 1; Length 39;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPPRFPFRFP 15

Db 25 RPPGFPPRFPFRFP 39

RESULT 3

US-08-310-722-1

; Sequence 1, Application US/08310722

; Patent No. 5654273

; GENERAL INFORMATION:

; APPLICANT: Gallo, Richard L.

; APPLICANT: Klagsbrun, Michael

; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 1100 Peachtree Street, Suite 2800

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30309-4530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/310,722

; FILING DATE: 22-SEP-1994

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: CMCC379

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-815-6508

; TELEFAX: (404)-815-6555

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; PUBLICATION INFORMATION:

; AUTHORS: Lee, Jong-Youn

; AUTHORS: Boman, Hans G.

; AUTHORS: Mutt, Viktor

; AUTHORS: Jornvall, Hans

; TITLE: No. 5654273el Polypeptides And Their Use

; JOURNAL: PCT WO 92/22578

; DATE: 12/23/92

; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39

US-08-310-722-1

Query Match 100.0%; Score 92; DB 1; Length 39;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPPRFPFRFP 15

Db 25 RPPGFPPRFPFRFP 39

RESULT 4

US-08-419-066-1

; Sequence 1, Application US/08419066

; Patent No. 5830993

; GENERAL INFORMATION:

; APPLICANT: Blecha, Frank

; APPLICANT: Shi, Jishu

; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &

; ADDRESSEE: Collins

; STREET: 2405 Grand Boulevard, Suite 400

; CITY: Kansas City

; STATE: Missouri

; COUNTRY: U.S.A.

; ZIP: 64108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/419,066

; FILING DATE:



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; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jornvall, Hans
; TITLE: No. 5863897el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-728-333-1

Query Match      100.0%; Score 92; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RPPGFPPRPFRFP 15
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Db      25 RPPGFPPRPFRFP 39

RESULT 6
US-09-024-975-1
; Sequence 1, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-975-1

Query Match      100.0%; Score 92; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RPPGFPPRPFRFP 15
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Db      25 RPPGFPPRPFRFP 39

RESULT 7

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US-08-930-777A-1  
; Sequence 1, Application US/08930777A  
; Patent No. 6713605  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-930-777A-1

Query Match 100.0%; Score 92; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRFPFRFP 15  
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Db 25 RPPGFPFRFPFRFP 39

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PCT-US95-12080-1  
; Sequence 1, Application PC/TUS9512080  
; GENERAL INFORMATION:  
; APPLICANT: Children's Medical Center Corporaton  
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
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; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/12080  
; FILING DATE:  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-873-8794  
; TELEFAX: (404)-815-8795  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; PUBLICATION INFORMATION:  
; AUTHORS: Lee, Jong-Youn  
; AUTHORS: Boman, Hans G.  
; AUTHORS: Mutt, Viktor  
; AUTHORS: Jornvall, Hans  
; TITLE: Novel Polypeptides And Their Use  
; JOURNAL: PCT WO 92/22578  
; DATE: 12/23/92  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39  
; PCT-US95-12080-1

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPPGFPFRFPFRFP 15  
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Db 25 RPPGFPFRFPFRFP 39

RESULT 9  
US-09-739-535-1  
; Sequence 1, Application US/09739535  
; Patent No. 6794490  
; GENERAL INFORMATION:  
; APPLICANT: Cubist Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS  
; FILE REFERENCE: C060  
; CURRENT APPLICATION NUMBER: US/09/739,535  
; CURRENT FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
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; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-09-739-535-1

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Db 25 RIPP-FPFRFPFRFP 38

RESULT 10  
US-08-487-359-5  
; Sequence 5, Application US/08487359  
; Patent No. 5633229  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADMIR N.  
; APPLICANT: HARWIG, SYLVIA S.L.  
; APPLICANT: LEHRER, ROBERT I.  
; TITLE OF INVENTION: PROPENINS-ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 9

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 2000 Pennsylvania Ave. N.W.  
;; CITY: Washington, D.C.  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 20006-1812  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/487,359  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/222,798  
;; FILING DATE: 05-APR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MURASHIGE, KATE H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 2000-0553.00  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 887-1500  
;; TELEFAX: (202) 887-0763  
;; TELEX: 90-4030  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 78 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-487-359-5  
  
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Best Local Similarity 78.6%; Pred. No. 1.2;  
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
  
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Db 34 PPQFPGPRFPFPP 47  
  
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; Sequence 5, Application US/08222798A  
; Patent No. 5804553  
; GENERAL INFORMATION:  
; APPLICANT: KOKRYAKOV, VLADIMIR N.  
; APPLICANT: HAWIG, SYLVIA S.L.  
; APPLICANT: LEHRER, ROBERT I.  
; TITLE OF INVENTION: PROPHENINS-ANTIBIOTIC PEPTIDES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave. N.W.  
; CITY: Washington, D.C.  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,798A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959

;; REFERENCE/DOCKET NUMBER: 2000-0553.00  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 887-1500  
;; TELEFAX: (202) 887-0763  
;; TELEX: 90-4030  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 78 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-222-798A-5  
  
Query Match 62.5%; Score 57.5; DB 1; Length 78;  
Best Local Similarity 78.6%; Pred. No. 1.2;  
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
  
QY 3 PPGFPP-PRFPFPP 15  
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Db 34 PPQFPGPRFPFPP 47  
  
RESULT 12  
US-09-024-975-3  
; Sequence 3, Application US/09024975  
; Patent No. 6133233  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, CHRISTOPHER R.  
; APPLICANT: BLECHA, FRANK  
; APPLICANT: SHI, JISHU  
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
; STREET: 2405 GRAND BLVD., SUITE 400  
; CITY: KANSAS CITY  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
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; APPLICATION NUMBER: US/09/024,975  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/802,306  
; FILING DATE: 18-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COLLINS, JOHN M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 25585-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 816/474-9050  
; TELEFAX: 816/474-9057  
; INFORMATION FOR SEQ ID NO: 3:  
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; LENGTH: 16 amino acids  
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Best Local Similarity 76.9%; Pred. No. 0.3;  
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;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
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US-08-419-066-2

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:05:05 ; Search time 55.3636 Seconds  
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Title: US-10-014-147-6  
Perfect score: 92  
Sequence: 1 RIPPGFPPRPPRP 15

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Searched: 1862994 seqs, 417510619 residues

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	92	100.0	39	15	US-10-391-155-2
6	92	100.0	39	15	US-10-391-155-6
7	92	100.0	39	15	US-10-391-155-1
8	92	100.0	42	16	US-10-344-709C-18
9	92	100.0	42	17	US-10-916-185-14
10	92	100.0	42	18	US-10-991-286A-44
11	92	100.0	42	20	US-11-004-379-20

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13	75.5	82.1	38	9	US-09-739-535-1	Sequence 1, Appli
14	60	65.2	103	15	US-10-424-599-258982	Sequence 258982,
15	59	64.1	103	15	US-10-424-599-211799	Sequence 211799,
16	59	64.1	107	15	US-10-424-599-208016	Sequence 208016,
17	58.5	63.6	101	16	US-10-425-115-322756	Sequence 322756,
18	57.5	62.5	366	16	US-10-408-765A-1261	Sequence 1261, Ap
19	57	62.0	16	14	US-10-014-147-5	Sequence 5, Appli
20	57	62.0	16	15	US-10-651-147-5	Sequence 5, Appli
21	57	62.0	23	14	US-10-014-147-3	Sequence 3, Appli
22	57	62.0	23	15	US-10-651-147-3	Sequence 3, Appli
23	57	62.0	26	14	US-10-014-147-2	Sequence 2, Appli
24	57	62.0	26	15	US-10-651-147-2	Sequence 2, Appli
25	56	60.9	125	16	US-10-437-963-113302	Sequence 113302,
26	56	60.9	153	16	US-10-425-115-268716	Sequence 268716,
27	56	60.9	304	14	US-10-156-761-13550	Sequence 13550, A
28	56	60.9	560	13	US-10-114-893-84	Sequence 84, Appl
29	56	60.9	615	16	US-10-425-115-319541	Sequence 319541,
30	56	60.9	2382	14	US-10-196-935A-2	Sequence 2, Appli
31	56	60.9	2382	15	US-10-052-648A-40	Sequence 40, Appl
32	56	60.9	2382	15	US-10-336-472-230	Sequence 230, App
33	56	60.9	2382	16	US-10-408-765A-1404	Sequence 1404, Ap
34	56	60.9	2382	20	US-11-009-554-8	Sequence 8, Appli
35	55.5	60.3	111	16	US-10-425-115-195600	Sequence 195600,
36	55	59.8	83	16	US-10-437-963-118176	Sequence 118176,
37	55	59.8	96	16	US-10-437-963-120965	Sequence 120965,
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39	55	59.8	143	15	US-10-424-599-189499	Sequence 189499,
40	55	59.8	171	16	US-10-437-963-111951	Sequence 111951,
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44	53.5	58.2	122	15	US-10-424-599-193533	Sequence 193533,
45	53	57.6	107	16	US-10-437-963-164555	Sequence 164555,

ALIGNMENTS

RESULT 1  
US-10-014-147-6  
; Sequence 6, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/014,147  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 15 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-10-014-147-6
      Query Match      100.0%;   Score 92;   DB 14;   Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 RPPGFPFRPPRFP 15

RESULT 2
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; Sequence 6, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
;           Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/651,147
; FILING DATE: 28-Aug-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 15 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-651-147-6
      Query Match      100.0%;   Score 92;   DB 15;   Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RPPGFPFRPPRFP 15
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```

```

Db      1 RPPGFPFRPPRFP 15

RESULT 3
US-10-014-147-1
; Sequence 1, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
;           Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 39 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-014-147-1
      Query Match      100.0%;   Score 92;   DB 14;   Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RPPGFPFRPPRFP 15
      |||||
Db      25 RPPGFPFRPPRFP 39

RESULT 4
US-10-391-155-1
; Sequence 1, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
;           Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
;           selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts

```

```

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-391-155-2

Query Match 100.0%; Score 92; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPPGFPFRFPFRFP 15
Db 25 RPPGFPFRFPFRFP 39

RESULT 6
US-10-391-155-6
; Sequence 6, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: Wordperfect version 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391.155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6

Query Match 100.0%; Score 92; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPPGFPFRFPFRFP 15
Db 25 RPPGFPFRFPFRFP 39

RESULT 7
US-10-651-147-1
; Sequence 1, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide

```

;
;
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/651,147
; FILING DATE: 28-Aug-2003
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-651-147-1

Query Match 100.0%; Score 92; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPPGFPPRPFRFP 15
Db 25 RPPGFPPRPFRFP 39

RESULT 8
US-10-344-709C-18
; Sequence 18, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; FILE REFERENCE: SONN:0300S
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-18
Query Match 100.0%; Score 92; DB 16; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RPPGFPPRPFRFP 15
Db 25 RPPGFPPRPFRFP 39

RESULT 9
US-10-916-185-14
; Sequence 14, Application US/10916185
; Publication No. US20050107325A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kesavan, Venkitasamy
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: MODIFIED iRNA AGENTS
; FILE REFERENCE: 14174-091001
; CURRENT APPLICATION NUMBER: US/10/916,185
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 60/510,246
; PRIOR FILING DATE: 2003-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-10-916-185-14

Query Match 100.0%; Score 92; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RPPGFPPRPFRFP 15
Db 25 RPPGFPPRPFRFP 39

RESULT 10
US-10-991-286A-44
; Sequence 44, Application US/10991286A
; Publication No. US20050186591A1
; GENERAL INFORMATION:
; APPLICANT: Bumcrot, David
; APPLICANT: Farrer, Matthew J.
; APPLICANT: Maraganore, Demetrius M.
; APPLICANT: Vornlocher, Hans-Peter
; TITLE OF INVENTION: METHOD OF TREATING NEURODEGENERATIVE DISEASE
; FILE REFERENCE: 17574-003001
; CURRENT APPLICATION NUMBER: US/10/991,286A
; CURRENT FILING DATE: 2004-11-17







; SEQ ID NO 258982  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_75885C.1.pep  
US-10-424-599-258982

Query Match 65.2%; Score 60; DB 15; Length 103;  
Best Local Similarity 66.7%; Pred. No. 6.3;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPPGFPFRPPRPF 15  
|:| | | | | | |  
Db 85 RVPFRVPPRGRVP 99

RESULT 15  
US-10-424-599-211799  
; Sequence 211799, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 211799  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_33281C.1.pep  
US-10-424-599-211799

Query Match 64.1%; Score 59; DB 15; Length 103;  
Best Local Similarity 78.6%; Pred. No. 8.2;  
Matches 11; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 3 PPGFP--PRFPRF 14  
| | | | | | |  
Db 27 PPGFPWPRIPRF 40

Search completed: October 26, 2005, 05:28:58  
Job time : 56.3636 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:51:43 ; Search time 55.1091 Seconds  
(without alignments)  
98.253 Million cell updates/sec

Title: US-10-014-147-7  
Perfect score: 83  
Sequence: 1 RRRPRPPYLPRRP 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	14	2 AAW01450	Aaw01450 Leukocyte
2	83	100.0	14	2 AAW75725	Aaw75725 Proline/A
3	83	100.0	14	8 ADE86118	Ade86118 Proline-a
4	83	100.0	14	8 ADL67260	Adl67260 Antimicro
5	83	100.0	15	3 AAB26885	Aab26885 PR-39 der
6	83	100.0	15	4 AAB97277	Aab97277 PR-39 der
7	83	100.0	15	4 AAB84691	Aab84691 Amino aci
8	83	100.0	19	2 AAW01452	Aaw01452 Leukocyte
9	83	100.0	19	8 ADE86115	Ade86115 Proline-a
10	83	100.0	19	8 ADL67257	Adl67257 Antimicro
11	83	100.0	26	2 AAW01447	Aaw01447 Leukocyte
12	83	100.0	26	2 AAW75723	Aaw75723 Proline/A
13	83	100.0	26	8 ADE86113	Ade86113 Proline-a
14	83	100.0	26	8 ADL67255	Adl67255 Antimicro
15	83	100.0	39	2 AAR30491	Aar30491 Antibacte
16	83	100.0	39	2 AAR99121	Aar99121 Magainin-
17	83	100.0	39	2 AAR94446	Aar94446 Synducin
18	83	100.0	39	2 AAW01446	Aaw01446 Leukocyte
19	83	100.0	39	2 AAW75722	Aaw75722 Proline/A
20	83	100.0	39	3 AAB26888	Aab26888 PR-39 pep
21	83	100.0	39	4 AAB97280	Aab97280 PR-39 pep
22	83	100.0	39	4 AAB84690	Aab84690 Amino aci
23	83	100.0	39	8 ADD35364	Add35364 Antimicro
24	83	100.0	39	8 ADE86112	Ade86112 Proline-a
25	83	100.0	39	8 ADL67254	Adl67254 Antimicro

26	83	100.0	42	5 ABB07714	Abb07714 Antimicro
27	83	100.0	42	8 ADR82250	Adr82250 Cell perm
28	83	100.0	44	4 AAB51194	Aab51194 E. coli A
29	68	81.9	23	2 AAW01451	Aaw01451 Leukocyte
30	68	81.9	23	8 ADE86114	Ade86114 Proline-a
31	68	81.9	23	8 ADL67256	Adl67256 Antimicro
32	66	79.5	18	2 AAR79211	Aar79211 Bacteneci
33	66	79.5	20	2 AAW75730	Aaw75730 Proline/A
34	66	79.5	23	2 AAR79209	Aar79209 Bacteneci
35	66	79.5	35	2 AAR79212	Aar79212 Bacteneci
36	66	79.5	59	2 AAW66400	Aaw66400 Cationic
37	66	79.5	59	3 AAY91699	Aay91699 Cationic
38	66	79.5	59	6 ABU59576	Abu59576 Cationic
39	66	79.5	60	5 ABB07713	Abb07713 Antimicro
40	66	79.5	62	4 AAB51197	Aab51197 E. coli A
41	64	77.1	11	3 AAB26886	Aab26886 PR-39 der
42	64	77.1	11	4 AAB97278	Aab97278 PR-39 der
43	64	77.1	11	4 AAB84692	Aab84692 Amino aci
44	64	77.1	11	6 ABG33050	Abg33050 Pig arg/p
45	64	77.1	11	7 ADB87318	Adb87318 Human pep

ALIGNMENTS

RESULT 1  
AAW01450.  
ID AAW01450 standard; peptide; 14 AA.  
XX  
AC AAW01450;  
XX  
DT 18-JUN-1997 (first entry)  
XX  
DE Leukocyte O2- production inhibitor peptide PR14.  
XX  
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;  
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;  
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;  
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;  
KW tissue damage; oxygen radical; inflammatory disease; therapy.  
XX  
OS Synthetic.  
XX  
PN WO9632129-A1.  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-US004674.  
XX  
PR 10-APR-1995; 95US-00419066.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 1996-476842/47.  
XX  
XX Inhibition of leukocyte super:oxide anion prodn. and attraction of  
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.  
XX  
PS Claim 12; Page 28; 45pp; English.  
XX  
CC AAW01447-W01454 represent fragments of the proline-arginine rich  
CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first  
CC isolated from porcine small intestine, and has also been identified in  
CC human and porcine neutrophils. PR39 kills bacteria by interfering with  
CC DNA and/or protein synthesis. PR39 also induces syndecan expression on  
CC mesenchymal cells. Syndecans are important in wound repair, showing that  
CC PR39 can be used in wound repair, as well as in antibacterial agents.  
CC These sequences, and PR39, can be used in the method of the invention.  
CC The method of the invention is for inhibiting leukocyte superoxide anion  
CC (O2-) production. The method comprises administering to a leukocyte a  
CC peptide (such as this sequence) capable of inhibiting leukocyte O2-

CC production. The peptides can be used as medicaments for fighting  
CC infection by attracting leukocytes to a wound site and restricting tissue  
CC damage at the wound site caused by excessive oxygen radicals produced by  
CC these leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states  
XX  
SQ Sequence 14 AA;  
  
Query Match 100.0%; Score 83; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RRRPRPPYLPRPRP 14  
Db 1 RRRPRPPYLPRPRP 14  
| | | | | | | | | | | | | | | |  
  
RESULT 2  
AAW75725  
ID AAW75725 standard; peptide; 14 AA.  
XX  
AC AAW75725;  
XX  
DT 19-NOV-1998 (first entry)  
XX  
DE Proline/Arginine rich peptide.  
XX  
KW Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;  
KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;  
KW coronary bypass; organ transplantation surgery.  
XX  
OS Synthetic.  
XX  
PN WO9835690-A1.  
XX  
PD 20-AUG-1998.  
XX  
PF 17-FEB-1998; 98WO-US003207.  
XX  
PR 18-FEB-1997; 97US-00802306.  
PR 16-FEB-1998; 98US-00024975.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
PI Ross CR, Blecha F, Shi J;  
XX  
DR WPI; 1998-495359/42.  
XX  
PT Reduction of reperfusion injury in temporarily occluded blood vessels -  
PT by administration of a peptide which is rich in proline or arginine  
PT residues.  
XX  
PS Claim 3; Page 15; 35pp; English.  
XX  
CC Sequences AAW75722-W75732 are proline/arginine rich peptides that upon  
CC administration into a mammal's bloodstream reduce reperfusion injury  
CC (production of reactive oxygen species, neutrophil adherence to  
CC endothelium, and extravasation of neutrophils). These peptides have two  
CC requirements: they contain the consensus sequence PXXP, where P is a  
CC proline residue and X is any amino acid residue, which has been found to  
CC inhibit superoxide production, and secondly they have arginine residues  
CC adjacent to these motifs, required for effective inhibition. It was  
CC established by structural and function analysis that a peptide should  
CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is  
CC correlated with the increase of length of peptides. The effectiveness of  
CC these peptides was determined by investigating the production of the  
CC neutrophil superoxide anion, and also the inhibition of neutrophil  
CC chemotaxis. From this, it was found that all of the peptides inhibited  
CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil  
CC oxidase activity. PR-39 is believed, to be the most potent endogenous  
CC down regulator of NADPH oxidase yet discovered, and from the data  
CC produced, it can be suggested to be involved in eliminating or reducing  
CC the reperfusion injury induced adhesion and extraction of neutrophils.

CC The peptides are also useful in connection with surgical procedures such  
CC as coronary bypass and organ transplantation surgery  
XX  
SQ Sequence 14 AA;  
  
Query Match 100.0%; Score 83; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RRRPRPPYLPRPRP 14  
Db 1 RRRPRPPYLPRPRP 14  
| | | | | | | | | | | | | | | |  
  
RESULT 3  
ADE86118  
ID ADE86118 standard; peptide; 14 AA.  
XX  
AC ADE86118;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Proline-arginine (PR)-rich antimicrobial peptide PR-14.  
XX  
KW Leukocyte superoxide anion; leukocyte O2- production;  
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;  
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;  
KW tissue damage; oxygen radical; antibacterial.  
XX  
OS Synthetic.  
XX  
PN US2003125249-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 07-DEC-2001; 2001US-00014147.  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 2004-059188/06.  
XX  
PT Attracting leukocyte to location by administering peptide including  
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to  
PT the location.  
XX  
PS Claim 3; SEQ ID NO 7; 24pp; English.  
XX  
CC The present invention relates to a method of inhibiting leukocyte  
CC superoxide anion (O2-) production and/or attracting leukocytes. The  
CC method comprises the use of proline-arginine (PR)-rich antimicrobial  
CC peptides or their truncated analogues. The method is useful for  
CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or  
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are  
CC useful as medicaments to fight infection by attracting leukocytes to a  
CC wound site, while restricting tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leukocytes. The present  
CC sequence represents a PR-rich antimicrobial peptide.  
XX  
SQ Sequence 14 AA;  
  
Query Match 100.0%; Score 83; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RRRPRPPYLPRPRP 14  
Db 1 RRRPRPPYLPRPRP 14  
| | | | | | | | | | | | | | | |

RESULT 4  
ADL67260  
ID ADL67260 standard; peptide; 14 AA.  
XX  
AC ADL67260;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39 analog PR-14.  
XX  
KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;  
antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;  
infection; wound; tissue damage; PR-39 analog; PR-14.  
XX  
OS Unidentified.  
XX  
PN US2004043934-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 28-AUG-2003; 2003US-00651147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX  
PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
PI Blecha F., Shi J;  
XX  
DR WPI; 2004-225728/21.  
XX

Inhibiting leukocyte oxygen radical production comprises contacting a leukocyte with a peptide, where the inhibition occurs as a consequence of binding between the peptide and p47phox.  
Example; SEQ ID NO 7; 24pp; English.

The invention relates to inhibiting leucocyte superoxide anion (O2-) production using a naturally occurring proline-arginine (PR)-rich antimicrobial peptide known as PR-39 and its truncated analogs. The method comprises contacting leucocytes with the peptide comprising 39 or 26 amino acids, for a time and under conditions effective to inhibit leucocyte superoxide anion production. The peptide inhibits the activity of NADPH oxidase responsible for anion production, by binding to Src homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein of the phagocytic NADPH oxidase complex. The leucocyte is a mammalian or porcine leucocyte and the mammalian leucocyte is neutrophil. Another method is also disclosed which employs a PR-39 analog that comprise 16 amino acids, where the sum of the proline and arginine residues in the effective peptide is at least 66 or 74 % of the total number of amino acids. This peptide inhibits leucocyte O2- production by the effective binding to p47phox in whole cells, therefore interfering with the binding of p47phox to p22phox. At least 14 or 25% of the amino acid residues in the peptide are arginine residues. The method of the invention is useful for inhibiting leucocyte oxygen radical production. The peptides are useful as medicaments for fighting infections by attracting leucocytes to a wound site, yet restrict tissue damage at the wound site caused by excessive oxygen radicals produced by these leucocytes. The present sequence is PR-39 analog, PR-14.

Sequence 14 AA;

Query Match 100.0%; Score 83; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLP RPRP 14

RESULT 5  
AAB26885  
ID AAB26885 standard; peptide; 15 AA.  
XX  
AC AAB26885;  
XX  
DT 01-FEB-2001 (first entry)  
XX  
DE PR-39 derived angiogenesis regulatory peptide 1.  
XX  
KW Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;  
myocardial ischaemia; proteasome.  
XX  
OS Synthetic.  
XX  
PN WO200057895-A1.  
XX  
PD 05-OCT-2000.  
XX  
PF 16-MAR-2000; 2000WO-US007050.  
XX  
PR 26-MAR-1999; 99US-00276868.  
XX  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Simons M, Gao Y;  
XX  
DR WPI; 2000-628319/60.  
XX  
PT Stimulating angiogenesis in situ, useful e.g. for treating anoxia and  
infarction, by administering a PR-39 oligopeptide that regulates  
enzymatic activity of proteasomes.  
XX  
PS Claim 12; Page 40; 51pp; English.  
XX  
CC This invention relates to a method for the stimulation of angiogenesis in  
situ within a targeted collection of viable cells. The method comprises  
introducing, into the cytoplasm, at least 1 member of the PR-39  
oligopeptide collective, which interacts with cytoplasmic proteasomes.  
CC Part of the proteolytic activity of the proteasomes is selectively  
altered so as to stimulate angiogenesis. The method is used to induce  
angiogenesis in tissue that has suffered anoxia or infarction, e.g.  
myocardial infarction or chronic myocardial ischaemia, and also to study  
the mechanisms that control angiogenesis. The present sequence represents  
a PR-39 derived peptide which interacts with the proteasome and can be  
used in the method of the invention  
XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLP RPRP 14

RESULT 6  
AAB97277  
ID AAB97277 standard; peptide; 15 AA.  
XX  
AC AAB97277;  
XX

DT 09-AUG-2001 (first entry)  
XX  
DE PR-39 derived peptide PR-15.  
XX

PR-39; cathelin; inflammation; wound healing; myocardial infarction;  
proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;  
anoxia; chronic myocardial ischaemia; heart tissue.

OS Unidentified.  
XX WO200130368-A1.  
PN  
XX  
PD 03-MAY-2001.  
XX  
PF 06-OCT-2000; 2000WO-US027552.  
XX  
PR 25-OCT-1999; 99US-00426011.  
XX  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
XX  
PI Simons M, Gao Y;  
XX  
DR WPI; 2001-355179/37.  
XX  
PT Stimulation of angiogenesis and inhibition of proteasome mediated  
PT degradation in cells, by introduction of PR-39 oligopeptide or its N-  
PT terminal fragments or their conjugates, for use in anoxia and infarction  
PT conditions.  
XX  
PS Claim 12; Page 42; 52pp; English.  
XX  
CC Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39  
CC is a member of the the cathelin family of proteins, mature PR-39 is 39  
CC amino acids in length (see AAB97280), and has been shown to play a role  
CC in several inflammatory events including wound healing and myocardial  
CC infarction. The PR-39 derived family of oligopeptides cause selective  
CC inhibition of proteasome mediated degeneration of peptides and  
CC stimulation of angiogenesis after their intracellular introduction to a  
CC target cell. PR-39 derived peptides are able to interact with at least  
CC the alpha7 subunit of the proteasomes, and therefore alter the  
CC proteolytic activity of the proteasomes, such that a selective increased  
CC expression of specific proteins occurs. The invention includes methods  
CC for the selective inhibition of proteasome mediated peptide degradation.  
CC The method provides means for stimulating angiogenesis as required in  
CC living tissues and organs which have suffered defects or have undergone  
CC anoxia and/or infarction, myocardial infarction or chronic myocardial  
CC ischaemia of heart tissue. Examples are the myocardium, skeletal or  
CC smooth muscle, artery or vein, lung, brain, kidney, spleen, liver,  
CC gastrointestinal or nerve tissues, limbs, and extremities. A particular  
CC example is after myocardial infarction or ischaemia  
XX  
SQ Sequence 15 AA;  
  
Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRRPRPPYLPRPRP 14  
| | | | | | | | | | | | | |  
Db 1 RRRPRPPYLPRPRP 14  
  
RESULT 7  
AAB84691  
ID AAB84691 standard; peptide; 15 AA.  
XX  
AC AAB84691;  
XX  
DT 17-SEP-2001 (first entry)  
XX  
DE Amino acid sequence of a PR-39 derived peptide (residues 1-15).  
XX  
KW PR-39; IkappaBalpha degradation; NFkappaB transcription factor;  
KW myocardial infarction; chronic myocardial ischemia; heart disease;  
KW anoxia.  
XX  
OS Unidentified.  
XX  
PN WO200147540-A1.  
XX  
PD 05-JUL-2001.

XX 27-DEC-2000; 2000WO-US035293.  
PF  
XX 29-DEC-1999; 99US-00474967.  
PR  
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
PA  
XX Simons M, Gao Y;  
PI  
XX WPI; 2001-441690/47.  
DR  
XX  
PT Selective inhibition of IkappaBalpha degradation within targeted viable  
PT cell collection, involves interacting PR-39 oligopeptide with  
PT IkappaBalpha and proteasomes, and altering proteolytic activity of  
PT proteasomes.  
XX  
PS Claim 11; Page 58; 69pp; English.  
XX  
CC The present sequence represents a PR-39 derived peptide. It is used for  
CC selective inhibition of IkappaBalpha degradation within a targeted cell  
CC collection in-situ. The method is useful for selectively inhibiting  
CC IkappaBalpha protein degradation in situ, decreasing the activity of  
CC NFkappaB transcription factor and selective control of NFkappaB-dependent  
CC gene expression in situ. The PR-39 derived peptides are useful in the  
CC treatment of myocardial infarction, chronic myocardial ischemia of heart  
CC disease and anoxia  
XX  
SQ Sequence 15 AA;  
  
Query Match 100.0%; Score 83; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RRRPRPPYLPRPRP 14  
| | | | | | | | | | | | | |  
Db 1 RRRPRPPYLPRPRP 14  
  
RESULT 8  
AAW01452  
ID AAW01452 standard; peptide; 19 AA.  
XX  
AC AAW01452;  
XX  
DT 18-JUN-1997 (first entry)  
XX  
DE Leukocyte O2- production inhibitor peptide PR19.  
XX  
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;  
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;  
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;  
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;  
KW tissue damage; oxygen radical; inflammatory disease; therapy.  
XX  
OS Synthetic.  
XX  
PN WO9632129-A1.  
XX  
PD 17-OCT-1996.  
XX  
PF 10-APR-1996; 96WO-US004674.  
XX  
PR 10-APR-1995; 95US-00419066.  
XX  
PA (UNIV ) UNIV KANSAS STATE RES FOUND.  
XX  
PI Blecha F, Shi J;  
XX  
DR WPI; 1996-476842/47.  
XX  
PT Inhibition of leukocyte super:oxide anion prodn. and attraction of  
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.  
XX



PS Disclosure; Page 27; 45pp; English.  
XX AAW01447-W01454 represent fragments of the proline-arginine rich  
CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first  
CC isolated from porcine small intestine, and has also been identified in  
CC human and porcine neutrophils. PR39 kills bacteria by interfering with  
CC DNA and/or protein synthesis. PR39 also induces syndecan expression on  
CC mesenchymal cells. Syndecans are important in wound repair, showing that  
CC PR39 can be used in wound repair, as well as in antibacterial agents.  
CC These sequences, and PR39, can be used in the method of the invention.  
CC The method of the invention is for inhibiting leukocyte superoxide anion  
CC (O2-) production. The method comprises administering to a leukocyte a  
CC peptide (such as this sequence) capable of inhibiting leukocyte O2-  
CC production. The peptides can be used as medicaments for fighting  
CC infection by attracting leukocytes to a wound site and restricting tissue  
CC damage at the wound site caused by excessive oxygen radicals produced by  
CC these leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states  
XX  
SQ Sequence 19 AA;

Query Match 100.0%; Score 83; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
Db 1 RRRPRPPYLPRRP 14

RESULT 9  
ADE86115  
ID ADE86115 standard; peptide; 19 AA.  
XX  
AC ADE86115;

XX 29-JAN-2004 (first entry)  
DT  
DE Proline-arginine (PR)-rich antimicrobial peptide PR-19.  
XX

KW Leukocyte superoxide anion; leukocyte O2- production;  
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;  
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;  
KW tissue damage; oxygen radical; antibacterial.  
XX  
OS Synthetic.  
XX  
XX US2003125249-A1.

XX 03-JUL-2003.  
PD  
PF 07-DEC-2001; 2001US-00014147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.

XX (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX  
XX Blecha F, Shi J;  
XX  
XX WPI; 2004-059188/06.

XX Attracting leukocyte to location by administering peptide including  
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to  
PT the location.  
XX  
XX Example; SEQ ID NO 4; 24pp; English.

XX The present invention relates to a method of inhibiting leukocyte  
CC superoxide anion (O2-) production and/or attracting leukocytes. The  
CC method comprises the use of proline-arginine (PR)-rich antimicrobial  
CC peptides or their truncated analogues. The method is useful for

CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or  
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are  
CC useful as medicaments to fight infection by attracting leukocytes to a  
CC wound site, while restricting tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leukocytes. The present  
CC sequence represents a PR-rich antimicrobial peptide.  
XX  
SQ Sequence 19 AA;

Query Match 100.0%; Score 83; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
Db 1 RRRPRPPYLPRRP 14

RESULT 10  
ADL67257  
ID ADL67257 standard; peptide; 19 AA.  
XX  
AC ADL67257;

XX 20-MAY-2004 (first entry)  
DT  
DE Antimicrobial peptide PR-39 analog PR-19.  
XX

KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;  
KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;  
KW infection; wound; tissue damage; PR-39 analog; PR-19.  
XX  
OS Unidentified.

XX US2004043934-A1.  
XX 04-MAR-2004.  
XX  
XX 28-AUG-2003; 2003US-00651147.

XX 10-APR-1995; 95US-00419066.  
XX 08-OCT-1997; 97US-00930777.

XX (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.

XX Blecha F, Shi J;  
XX  
XX WPI; 2004-225728/21.

XX Inhibiting leukocyte oxygen radical production comprises contacting a  
PT leukocyte with a peptide, where the inhibition occurs as a consequence of  
PT binding between the peptide and p47phox.

XX Example; SEQ ID NO 4; 24pp; English.

XX The invention relates to inhibiting leukocyte superoxide anion (O2-)  
CC production using a naturally occurring proline-arginine (PR)-rich  
CC antimicrobial peptide known as PR-39 and its truncated analogs. The  
CC method comprises contacting leukocytes with the peptide comprising 39 or  
CC 26 amino acids, for a time and under conditions effective to inhibit  
CC leukocyte superoxide anion production. The peptide inhibits the activity  
CC of NADPH oxidase responsible for anion production, by binding to Src  
CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein  
CC of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or  
CC porcine leukocyte and the mammalian leukocyte is neutrophil. Another  
CC method is also disclosed which employs a PR-39 analog that comprise 16  
CC amino acids, where the sum of the proline and arginine residues in the  
CC effective peptide is at least 66 or 74 % of the total number of amino  
CC acids. This peptide inhibits leukocyte O2- production by the effective  
CC binding to p47phox in whole cells, therefore interfering with the binding  
CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in  
CC the peptide are arginine residues. The method of the invention is useful

CC for inhibiting leucocyte oxygen radical production. The peptides are  
CC useful as medicaments for fighting infections by attracting leucocytes to  
CC a wound site, yet restrict tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leucocytes. The present  
CC sequence is PR-39 analog, PR-19.  
XX  
SQ Sequence 19 AA;

Query Match 100.0%; Score 83; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLPRRP 14

RESULT 11  
AAW01447  
ID AAW01447 standard; peptide; 26 AA.  
XX  
AC AAW01447;

DT 18-JUN-1997 (first entry)  
XX  
DE Leukocyte O2- production inhibitor peptide PR26.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;  
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;  
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;  
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;  
KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.  
OS  
XX WO9632129-A1.  
PN  
XX 17-OCT-1996.

PD  
XX 10-APR-1996; 96WO-US004674.  
PF  
XX 10-APR-1995; 95US-00419066.

PR (UNIV ) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;  
PI  
XX WPI; 1996-476842/47.

DR  
XX Inhibition of leukocyte super:oxide anion prodn. and attraction of  
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39.

XX Claim 3; Page 26; 45pp; English.

PS  
XX AAW01447-W01454 represent fragments of the proline-arginine rich  
CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first  
CC isolated from porcine small intestine, and has also been identified in  
CC human and porcine neutrophils. PR39 kills bacteria by interfering with  
CC DNA and/or protein synthesis. PR39 also induces syndecan expression on  
CC mesenchymal cells. Syndecans are important in wound repair, showing that  
CC PR39 can be used in wound repair, as well as in antibacterial agents.  
CC These sequences, and PR39, can be used in the method of the invention.  
CC The method of the invention is for inhibiting leukocyte superoxide anion  
CC (O2-) production. The method comprises administering to a leukocyte a  
CC peptide (such as this sequence) capable of inhibiting leukocyte O2-  
CC production. The peptides can be used as medicaments for fighting  
CC infection by attracting leukocytes to a wound site and restricting tissue  
CC damage at the wound site caused by excessive oxygen radicals produced by  
CC these leukocytes. They can also be used to develop products for treating  
CC inflammatory disease states

XX Sequence 26 AA;

Query Match 100.0%; Score 83; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLPRRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLPRRP 14

RESULT 12  
AAW75723  
ID AAW75723 standard; peptide; 26 AA.

XX AAW75723;  
AC  
XX 19-NOV-1998 (first entry)  
DT  
XX

DE Proline/Arginine rich peptide PR-26.

XX Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;  
KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;  
KW coronary bypass; organ transplantation surgery.

XX Synthetic.  
OS  
XX WO9835690-A1.  
PN  
XX 20-AUG-1998.  
PD  
XX 17-FEB-1998; 98WO-US003207.  
PF  
XX 18-FEB-1997; 97US-00802306.  
PR  
XX 16-FEB-1998; 98US-00024975.

XX (UNIV ) UNIV KANSAS STATE RES FOUND.  
PA  
XX Ross CR, Blecha F, Shi J;  
PI  
XX WPI; 1998-495359/42.  
DR

XX Reduction of reperfusion injury in temporarily occluded blood vessels -  
PT by administration of a peptide which is rich in proline or arginine  
PT residues.

XX Claim 3; Page 14-15; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon  
CC administration into a mammal's bloodstream reduce reperfusion injury  
CC (production of reactive oxygen species, neutrophil adherence to  
CC endothelium, and extravasation of neutrophils). These peptides have two  
CC requirements: they contain the consensus sequence PXXP, where P is a  
CC proline residue and X is any amino acid residue, which has been found to  
CC inhibit superoxide production, and secondly they have arginine residues  
CC adjacent to these motifs, required for effective inhibition. It was  
CC established by structural and function analysis that a peptide should  
CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is  
CC correlated with the increase of length of peptides. The effectiveness of  
CC these peptides was determined by investigating the production of the  
CC neutrophil superoxide anion, and also the inhibition of neutrophil  
CC chemotaxis. From this, it was found that all of the peptides inhibited  
CC NADPH oxidase to some extent. All of the peptides also inhibit neutrophil  
CC oxidase activity. PR-39 is believed, to be the most potent endogenous  
CC down regulator of NADPH oxidase yet discovered, and from the data  
CC produced, it can be suggested to be involved in eliminating or reducing  
CC the reperfusion injury induced adhesion and extraction of neutrophils.  
CC The peptides are also useful in connection with surgical procedures such  
CC as coronary bypass and organ transplantation surgery

XX Sequence 26 AA;

Query Match 100.0%; Score 83; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLPRRP 14

RESULT 13  
ADE86113  
ID ADE86113 standard; peptide; 26 AA.  
XX  
AC ADE86113;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Proline-arginine (PR)-rich antimicrobial peptide PR-26.  
XX

KW Leukocyte superoxide anion; leukocyte O2- production;  
KW leukocyte attraction; proline-arginine-rich antimicrobial peptide;  
KW PR-rich antimicrobial peptide; neutrophil; wound site; infection;  
KW tissue damage; oxygen radical; antibacterial.  
XX

OS Synthetic.  
XX  
PN US2003125249-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 07-DEC-2001; 2001US-00014147.  
XX  
PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX

PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX

PI Blecha F, Shi J;  
XX  
DR WPI; 2004-059188/06.  
XX

XX Attracting leukocyte to location by administering peptide including  
PT proline-arginine-rich antimicrobial peptide or its truncated analogs to  
PT the location.  
XX

PS Claim 3; SEQ ID NO 2; 24pp; English.  
XX

CC The present invention relates to a method of inhibiting leukocyte  
CC superoxide anion (O2-) production and/or attracting leukocytes. The  
CC method comprises the use of proline-arginine (PR)-rich antimicrobial  
CC peptides or their truncated analogues. The method is useful for  
CC attracting a leukocyte e.g. a mammalian leukocyte, porcine leukocyte, or  
CC a neutrophil, to a location, e.g. a wound site. The PR-rich peptides are  
CC useful as medicaments to fight infection by attracting leukocytes to a  
CC wound site, while restricting tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leukocytes. The present  
CC sequence represents a PR-rich antimicrobial peptide.  
XX

SQ Sequence 26 AA;  
XX

Query Match 100.0%; Score 83; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLPRRP 14

RESULT 14  
ADL67255  
ID ADL67255 standard; peptide; 26 AA.  
XX  
AC ADL67255;  
XX

DT 20-MAY-2004 (first entry)  
XX  
DE Antimicrobial peptide PR-39 analog PR-26.  
XX  
KW Leucocyte; superoxide anion; oxygen radical; proline-arginine;  
KW antimicrobial; antioxidant; NADPH oxidase; p47phox; neutrophil;  
KW infection; wound; tissue damage; PR-39 analog; PR-26.  
XX  
OS Unidentified.  
XX

FH Location/Qualifiers  
FT 1. .3  
FT /note= "Essential for antibacterial activity"  
FT 20. .26  
FT /note= "Essential for antibacterial activity"  
XX

PN US2004043934-A1.  
XX

PD 04-MAR-2004.  
XX

PF 28-AUG-2003; 2003US-00651147.  
XX

PR 10-APR-1995; 95US-00419066.  
PR 08-OCT-1997; 97US-00930777.  
XX

PA (BLEC/) BLECHA F.  
PA (SHIJ/) SHI J.  
XX

PI Blecha F, Shi J;  
XX

DR WPI; 2004-225728/21.  
XX

XX Inhibiting leukocyte oxygen radical production comprises contacting a  
PT leukocyte with a peptide, where the inhibition occurs as a consequence of  
PT binding between the peptide and p47phox.  
XX

PS Claim 1; SEQ ID NO 2; 24pp; English.  
XX

CC The invention relates to inhibiting leukocyte superoxide anion (O2-)  
CC production using a naturally occurring proline-arginine (PR)-rich  
CC antimicrobial peptide known as PR-39 and its truncated analogs. The  
CC method comprises contacting leukocytes with the peptide comprising 39 or  
CC 26 amino acids, for a time and under conditions effective to inhibit  
CC leukocyte superoxide anion production. The peptide inhibits the activity  
CC of NADPH oxidase responsible for anion production, by binding to Src  
CC homology 3 (SH3) domain of p47phox, which is a 47 kDa cytosolic protein  
CC of the phagocytic NADPH oxidase complex. The leukocyte is a mammalian or  
CC porcine leukocyte and the mammalian leukocyte is neutrophil. Another  
CC method is also disclosed which employs a PR-39 analog that comprise 16  
CC amino acids, where the sum of the proline and arginine residues in the  
CC effective peptide is at least 66 or 74 % of the total number of amino  
CC acids. This peptide inhibits leukocyte O2- production by the effective  
CC binding to p47phox in whole cells, therefore interfering with the binding  
CC of p47phox to p22phox. At least 14 or 25% of the amino acid residues in  
CC the peptide are arginine residues. The method of the invention is useful  
CC for inhibiting leukocyte oxygen radical production. The peptides are  
CC useful as medicaments for fighting infections by attracting leukocytes to  
CC a wound site, yet restrict tissue damage at the wound site caused by  
CC excessive oxygen radicals produced by these leukocytes. The present  
CC sequence is PR-39 analog PR-26.  
XX

SQ Sequence 26 AA;  
XX

Query Match 100.0%; Score 83; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLPRRP 14

RESULT 15

AAR30491  
ID AAR30491 standard; peptide; 39 AA.  
XX  
AC AAR30491;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-MAY-1993 (first entry)  
XX  
DE Antibacterial peptide.  
XX  
KW Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;  
KW veterinary medicine; prophylactic.  
XX  
OS Sus scrofa domestica.  
XX  
PN WO9222578-A1.  
XX  
PD 23-DEC-1992.  
XX  
PF 10-JUN-1992; 92WO-SE000394.  
XX  
PR 14-JUN-1991; 91SE-00001838.  
XX  
PA (LEEJ/) LEE J.  
PA (BOMA/) BOMAN H G.  
PA (MUTT/) MUTT V.  
PA (JOER/) JOERNVALL H.  
XX  
PI Lee J, Boman HG, Mutt V, Joernvall H;  
XX  
DR WPI; 1993-018080/02.  
XX  
PT New anti-bacterial polypeptide - active against Gram negative bacteria.  
XX  
PS Claim 1; Page 10; 15pp; English.  
XX  
CC This peptide was isolated from the small intestine of a pig. The small  
CC intestine is an important endocrine organ and many physiologically active  
CC peptides have been isolated from it. This peptide inhibits the growth of,  
CC and may kill, bacteria, pref. gram negative bacteria. This peptide or its  
CC functional derivatives may be used in human or veterinary medicine for  
CC therapeutic or prophylactic use. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 39 AA;  
  
Query Match 100.0%; Score 83; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.0031;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RRRPRPPYLP RRP 14  
Db 1 RRRPRPPYLP RRP 14  
  
Search completed: October 26, 2005, 05:12:08  
Job time : 55.1091 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:00:14 ; Search time 10.4364 Seconds  
(without alignments)  
129.071 Million cell updates/sec

Title: US-10-014-147-7  
Perfect score: 83  
Sequence: 1 RRRPRPPYLP RRP 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	83	100.0	172	2	S68232 antimicrobial prot
2	66	79.5	59	2	A36589 bactenecin 7 - bov
3	58	69.9	190	2	S68230 antimicrobial pept
4	53	63.9	184	2	T29373 hypothetical prote
5	52.5	63.3	82	2	A41051 spore coat protein
6	52	62.7	1006	2	G86292 hypothetical prote
7	51.5	62.0	1187	1	JC4155 protein-tyrosine-p
8	51.5	62.0	1189	1	JC2366 protein-tyrosine-p
9	50	60.2	192	2	S76867 hypothetical prote
10	49.5	59.6	168	2	S35330 apidaecin 14 precu
11	49.5	59.6	199	2	S14981 extensin class I (
12	49	59.0	210	2	T33700 hypothetical prote
13	49	59.0	218	2	T22261 hypothetical prote
14	49	59.0	589	2	T29299 hypothetical prote
15	48	57.8	134	2	AC0665 probable cytochrom
16	48	57.8	139	4	S09612 hypothetical XrepB
17	48	57.8	261	1	WMBEXE infected cell prot
18	48	57.8	402	1	VGBE50 glycoprotein D pre
19	48	57.8	437	2	A88942 protein R13D11.3 l
20	48	57.8	520	2	T04591 ferulate-5-hydroxy
21	47.5	57.2	301	2	JQ1663 hybrid proline-ric
22	47	56.6	196	2	B48232 cysteine-rich exte
23	47	56.6	209	2	A48232 cysteine-rich exte
24	47	56.6	258	2	S55036 tyrosine-rich hydr
25	47	56.6	359	2	T13478 hypothetical prote
26	47	56.6	427	2	T32652 hypothetical prote
27	47	56.6	456	2	T35474 50kD proline rich
28	47	56.6	665	2	D96621 auxin response fac
29	47	56.6	693	2	JN0673 ubiquitin-like fus

30	47	56.6	701	2	JN0674 ubiquitin-like fus
31	47	56.6	751	2	T46517 hypothetical prote
32	47	56.6	846	1	QQBEC3 HQRF1 protein - hu
33	47	56.6	1085	2	S40476 Ca(2+)-sensing rec
34	46.5	56.0	752	2	G69457 ribonucleoside-dip
35	46.5	56.0	818	2	T02436 proline-rich prote
36	46	55.4	26	2	S06675 apidaecin 1b precu
37	46	55.4	144	2	S35331 apidaecin 22 precu
38	46	55.4	160	2	C72501 hypothetical prote
39	46	55.4	180	2	S43791 PBDX protein - hum
40	46	55.4	188	2	B85737 cytochrome b(561)
41	46	55.4	188	2	G90881 cytochrome b(561)
42	46	55.4	188	2	E64893 cytochrome b561 -
43	46	55.4	264	2	T51304 splicing factor RS
44	46	55.4	271	2	T47978 splicing factor RS
45	46	55.4	283	2	S35332 apidaecin 73 precu

ALIGNMENTS

RESULT 1

S68232 antimicrobial protein PR-39 precursor, cathelin-associated - pig  
N;Alternate names: myeloid antibacterial protein PR-39  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S68232; JN0899; I47138; S19563  
R;Zhao, C.; Ganz, T.; Lehrer, R.I.  
FEBS Lett. 376, 130-134, 1995  
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni  
A;Reference number: S68232; MUID:96105365; PMID:7498526  
A;Accession: S68232  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-172 <ZHA>  
A;Cross-references: UNIPROT:P80054; EMBL:X89201; NID:gl165150; PIDN:CAA61487.1; PID:gl166  
A;Experimental source: leukocytes  
R;Storici, P.; Zanetti, M.  
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993  
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i  
A;Reference number: JN0899; MUID:94071853; PMID:8250863  
A;Accession: JN0899  
A;Molecule type: mRNA  
A;Residues: 1-20,'A',22-172 <STO>  
A;Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101  
A;Experimental source: bone marrow cells  
R;Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bome  
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995  
A;Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami  
A;Reference number: I47138; MUID:95350216; PMID:7624374  
A;Accession: I47138  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-28,'T',30-89,'QR',92-116,'NDP',120-172 <GUD>  
A;Cross-references: EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PID:gl051298  
R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,  
Eur. J. Biochem. 202, 849-854, 1991  
A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of ti  
A;Reference number: S19563; MUID:92111534; PMID:1765098  
A;Accession: S19563  
A;Molecule type: protein  
A;Residues: 131-169 <AGE>  
A;Experimental source: intestine  
C;Genetics:  
A;Gene: PR39  
A;Introns: 66/3; 102/3; 126/3  
C;Superfamily: cathelin; cystatin homology  
C;Keywords: amidated carboxyl end; antibacterial  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;22-129/Domain: cystatin homology <CYS>  
F;30-130/Domain: propeptide #status predicted <PRO>  
F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>



F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 100.0%; Score 83; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
| | | | | | | | | |  
Db 131 RRRPRPPYLPRRP 144

RESULT 2  
A36589  
bactenecin 7 - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-May-1997  
C;Accession: A36589  
R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.  
J. Biol. Chem. 265, 18871-18874, 1990  
A;Title: Amino acid sequences of two proline-rich bacterenecins. Antimicrobial peptides of  
A;Reference number: A36589; MUID:91035404; PMID:2229048  
A;Accession: A36589  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-59 <FRA>  
C;Superfamily: cathelin; cystatin homology

Query Match 79.5%; Score 66; DB 2; Length 59;  
Best Local Similarity 85.7%; Pred. No. 0.033;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
| | | | | | | | | |  
Db 2 RIRPRPPRLPRRP 15

RESULT 3  
S68230  
antimicrobial peptide precursor - sheep  
N;Alternate names: Bac7.5 peptide homolog  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S68230  
R;Bagella, L.; Scocchi, M.; Zanetti, M.  
FEBS Lett. 376, 225-228, 1995  
A;Title: cDNA sequences of three sheep myeloid cathelicidins.  
A;Reference number: S68228; MUID:96105386; PMID:7498547  
A;Accession: S68230  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-190 <BAG>  
A;Cross-references: UNIPROT:P50415; EMBL:L46852; NID:g1161244; PIDN:AAA85468.1; PID:g116  
C;Superfamily: cathelin; cystatin homology  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;22-129/Domain: cystatin homology <CYS>  
F;29-130/Domain: propeptide #status predicted <PRO>  
F;130-190/Product: antimicrobial peptide #status predicted <MAT>

Query Match 69.9%; Score 58; DB 2; Length 190;  
Best Local Similarity 78.6%; Pred. No. 1.1;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
| | | | | | | | | |  
Db 132 RLRPRRRLPRRP 145

RESULT 4  
T29373  
hypothetical protein ZC404.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T29373

R;Bentley, D.; Le, T.T.  
submitted to the EMBL Data Library, April 1996  
A;Description: The sequence of C. elegans cosmid ZC404.  
A;Reference number: Z20614  
A;Accession: T29373  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-184 <BEN>  
A;Cross-references: UNIPROT:Q23291; EMBL:U55363; PIDN:AAA97967.1; GSPDB:GN00023; CESP:ZC4  
A;Experimental source: strain Bristol N2; clone ZC404  
C;Genetics:  
A;Gene: CESP:ZC404.1  
A;Map position: 5  
A;Introns: 15/2; 50/2; 75/2; 138/2  
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC404.1

Query Match 63.9%; Score 53; DB 2; Length 184;  
Best Local Similarity 90.0%; Pred. No. 4.4;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RPRPPYLPRP 12  
| | | | | | | | | |  
Db 26 RPRKPYLPRP 35

RESULT 5  
A41051  
spore coat protein precursor - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 03-Apr-1992 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S04835; A41051; F69606  
R;Aronson, A.I.; Song, H.Y.; Bourne, N.  
Mol. Microbiol. 3, 437-444, 1989  
A;Title: Gene structure and precursor processing of a novel Bacillus subtilis spore coat  
A;Reference number: S04835; MUID:89313296; PMID:2546006  
A;Accession: S04835  
A;Molecule type: DNA  
A;Residues: 'MNVHTPNLSIRNMVKGIKKAREVPLL', 2-82 <AR2>  
A;Cross-references: UNIPROT:P11863; EMBL:X13740; NID:g39864; PIDN:CAA32004.1; PID:g39865  
A;Experimental source: strain JH642  
A;Note: part of this sequence, including the amino end of the mature protein, was confirm  
R;Bourne, N.; FitzJames, P.C.; Aronson, A.I.  
J. Bacteriol. 173, 6618-6625, 1991  
A;Title: Structural and germination defects of Bacillus subtilis spores with altered cont  
A;Reference number: A41051; MUID:92011439; PMID:1917883  
A;Accession: A41051  
A;Molecule type: protein  
A;Residues: 'XX', 3-11 <BOU>  
A;Experimental source: strain JH642  
A;Note: the material sequenced was the larger of two isolated precursor forms; the amino  
A;Note: both the location of the transcription start site and peptide sequencing of the  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choj  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;  
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: F69606  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 'MNVHTPNLSIRNMVKGIKKAREVPLL', 2-82 <KUN>  
A;Cross-references: GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13066.1; PID:g2633563  
A;Experimental source: strain 168

C;Comment: This structural protein is expressed during stage V of sporulation.

C;Genetics:  
A;Gene: CotT  
A;Start codon: TTG  
C;Keywords: sporulation  
F;1-19/Domain: propeptide #status experimental <PRO>  
F;20-82/Product: spore coat protein #status experimental <MAT>

Query Match 63.3%; Score 52.5; DB 2; Length 82;  
Best Local Similarity 83.3%; Pred. No. 2.3;  
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 4 PRPP-YLPRPRP 14  
||| | ||||  
Db 49 PRPPYYPRPRP 60

RESULT 6

G86292  
hypothetical protein F7H2.17 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: G86292  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: G86292  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1006 <STO>  
A;Cross-references: UNIPROT:Q9LMQ1; GB:AE005172; NID:g8927662; PIDN:AAF82153.1; GSPDB:GN  
C;Genetics:  
A;Map position: 1

Query Match 62.7%; Score 52; DB 2; Length 1006;  
Best Local Similarity 81.8%; Pred. No. 31;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PRPP-YLPRPRP 14  
||| | ||||  
Db 99 PRPPRPRPRP 109

RESULT 7

JC4155  
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - human  
N;Alternate names: PEZ protein; protein-tyrosine-phosphatase/ezrin-like protein  
C;Species: Homo sapiens (man)  
C;Date: 27-Aug-1995 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: JC4155  
R;Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, M.R Biochem. Biophys. Res. Commun. 209, 959-965, 1995  
A;Title: PEZ: a novel human cDNA encoding protein tyrosine phosphatase-and ezrin-like dom  
A;Reference number: JC4155; MUID:95251727; PMID:7733990  
A;Accession: JC4155  
A;Molecule type: mRNA  
A;Residues: 1-1187 <SMI>  
A;Cross-references: UNIPROT:Q15678; EMBL:X82676; NID:g3929753; PIDN:CAA57993.1; PID:g809  
A;Experimental source: breast  
C;Genetics:  
A;Gene: GDB:PTPN14  
A;Cross-references: GDB:454485  
A;Map position: 1q32.2-1q32.2  
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b  
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatad

F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41>  
F;566-575/Region: proline-rich  
F;709-716/Region: acidic  
F;933-1169/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F;1121/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1127/Binding site: substrate phosphate (Arg) #status predicted

Query Match 62.0%; Score 51.5; DB 1; Length 1187;  
Best Local Similarity 83.3%; Pred. No. 42;  
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 RPRPPYLPRPRP 14  
|| | || ||||  
Db 565 RPPPPY-PRPRP 575

RESULT 8

JC2366  
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse  
N;Alternate names: PEZ protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-phos  
C;Species: Mus musculus (house mouse)  
C;Date: 24-Feb-1995 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: JC2366  
R;Sawada, M.; Ogata, M.; Fujino, Y.; Hamaoka, T.  
Biochem. Biophys. Res. Commun. 203, 479-484, 1994  
A;Title: cDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskelet  
A;Reference number: JC2366; MUID:94354845; PMID:8074693  
A;Accession: JC2366  
A;Molecule type: mRNA  
A;Residues: 1-1189 <SAW>  
A;Cross-references: UNIPROT:Q62130; GB:D31842; NID:g507330; PIDN:BAA06628.1; PID:g507331  
A;Experimental source: thymus  
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-bj  
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41>  
F;566-575/Region: proline-rich  
F;712-718/Region: acidic  
F;935-1171/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F;1123/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1129/Binding site: substrate phosphate (Arg) #status predicted

Query Match 62.0%; Score 51.5; DB 1; Length 1189;  
Best Local Similarity 83.3%; Pred. No. 42;  
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 RPRPPYLPRPRP 14  
|| | || ||||  
Db 565 RPPPPY-PRPRP 575

RESULT 9

S76867  
hypothetical protein - Synechocystis sp. (strain PCC 6803)  
C;Species: Synechocystis sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S76867  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
S.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S76867  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-192 <KAN>  
A;Cross-references: UNIPROT:P74661; EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA1877;  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 60.2%; Score 50; DB 2; Length 192;  
Best Local Similarity 69.2%; Pred. No. 11;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RRRPPPYLPRPRP 14  
| | | | | | | |  
Db 3 RRRPPRYTPPRP 15  
| | | | | | | |  
RESULT 10  
S35330  
apidaecin 14 precursor - honeybee  
N;Contains: apidaecin II  
C;Species: Apis mellifera (honeybee)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: S35330; S06676  
R;Casteels-Josson, K.; Capaci, T.; Casteels, P.; Tempst, P.  
EMBO J. 12, 1569-1578, 1993  
A;Title: Apidaecin multipeptide precursor structure: a putative mechanism for amplification  
A;Reference number: S35330; MUID:93223697; PMID:8467807  
A;Accession: S35330  
A;Molecule type: mRNA  
A;Residues: 1-168 <CAS>  
A;Cross-references: UNIPROT:Q06601; EMBL:X72575; NID:g297062; PIDN:CAA51167.1; PID:g297062  
R;Casteels, P.; Ampe, C.; Jacobs, F.; Vaeck, M.; Tempst, P.  
EMBO J. 8, 2387-2391, 1989  
A;Title: Apidaecins: antibacterial peptides from honeybees.  
A;Reference number: S05383; MUID:90005446; PMID:2676519  
A;Accession: S06676  
A;Molecule type: protein  
A;Residues: 43-60 <CA2>  
C;Superfamily: procyclic acidic repetitive protein  
F;43-60/Product: apidaecin II #status experimental <MAT>  
Query Match 59.6%; Score 49.5; DB 2; Length 168;  
Best Local Similarity 47.6%; Pred. No. 11;  
Matches 10; Conservative 2; Mismatches 2; Indels 7; Gaps 1;  
QY 1 RRRP-----RPPYLPRPRP 14  
| | | | | | | |  
Db 117 RREPAEPGNRPVYIPQPRP 137  
| | | | | | | |  
RESULT 11  
S14981  
extensin class I (clone wl-8 L) - tomato (fragment)  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 11-Jan-2000  
C;Accession: S14981  
R;Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.  
Plant Mol. Biol. 16, 547-565, 1991  
A;Title: Tomato extensin and extensin-like cDNAs: structure and expression in response to wounding  
A;Reference number: S14970; MUID:91329690; PMID:1714316  
A;Accession: S14981  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-199 <SHO>  
A;Cross-references: EMBL:X55692  
A;Experimental source: cv. UC82B  
C;Superfamily: hydroxyproline-rich glycoprotein  
C;Keywords: cell wall; glycoprotein; hydroxyproline  
Query Match 59.6%; Score 49.5; DB 2; Length 199;  
Best Local Similarity 71.4%; Pred. No. 13;  
Matches 10; Conservative 0; Mismatches 1; Indels 3; Gaps 1;  
QY 4 PRPP---YLP RPRP 14  
| | | | | | | |  
Db 77 PRPPPEYLP RPRP 90  
| | | | | | | |  
RESULT 12  
T33700  
hypothetical protein F49F1.9 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T33700  
R;Miller, N.; Wamsley, P.  
submitted to the EMBL Data Library, October 1998  
A;Description: The sequence of C. elegans cosmid F49F1.  
A;Reference number: Z21389  
A;Accession: T33700  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-210 <MIL>  
A;Cross-references: UNIPROT:Q9GZE0; EMBL:AF100656; PIDN:AAC68952.1; GSPDB:GN00022; CESP:F49F1  
A;Experimental source: strain Bristol N2; clone F49F1  
C;Genetics:  
A;Gene: CESP:F49F1.9  
A;Map position: 4  
A;Introns: 130/3

Query Match 59.0%; Score 49; DB 2; Length 210;  
Best Local Similarity 69.2%; Pred. No. 16;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RRRPPPYLPRPRP 14  
| | | | | | | |  
Db 53 RPPRPPRPPRPTP 65  
| | | | | | | |

RESULT 13  
T22261  
hypothetical protein F46A8.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T22261  
R;Harris, B.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19539  
A;Accession: T22261  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-218 <WIL>  
A;Cross-references: UNIPROT:O01331; EMBL:Z81539; PIDN:CAB04391.1; GSPDB:GN00019; CESP:F46A8  
A;Experimental source: clone F46A8  
C;Genetics:  
A;Gene: CESP:F46A8.5  
A;Map position: 1  
A;Introns: 138/3

Query Match 59.0%; Score 49; DB 2; Length 218;  
Best Local Similarity 69.2%; Pred. No. 17;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RRRPPPYLPRPRP 14  
| | | | | | | |  
Db 61 RPPRPPRPPRPTP 73  
| | | | | | | |

RESULT 14  
T29299  
hypothetical protein C50F7.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T29299  
R;Johnson, D.; Stellyes, L.  
submitted to the EMBL Data Library, November 1995  
A;Description: The sequence of C. elegans cosmid C50F7.  
A;Reference number: Z20601  
A;Accession: T29299  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-589 <JOH>  
A;Cross-references: UNIPROT:Q18756; EMBL:U41557; PIDN:AAA83307.1; CESP:C50F7.2  
C;Genetics:  
A;Gene: CESP:C50F7.2  
A;Introns: 12/2  
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

Query Match 59.0%; Score 49; DB 2; Length 589;  
Best Local Similarity 81.8%; Pred. No. 44;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RRRPPYLRP 12  
| | | | |  
Db 105 RRRPTRLRP 115

RESULT 15  
AC0665  
probable cytochrome STY1431 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AC0665  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Karpman, A.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, M.; S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AC0665  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-134 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD01692.1; PID:gl6502543; GSPDB:GN00176  
C;Genetics:  
A;Gene: STY1431

Query Match 57.8%; Score 48; DB 2; Length 134;  
Best Local Similarity 63.6%; Pred. No. 14;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PRPPYLRP 14  
| | | | : | | : |  
Db 25 PTPPIVPRPKP 35

Search completed: October 26, 2005, 05:20:02  
Job time : 11.4364 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 04:52:03 ; Search time 48.4909 Seconds  
(without alignments)  
147.844 Million cell updates/sec

Title: US-10-014-147-7  
Perfect score: 83  
Sequence: 1 RRRPRPPYLPRPRP 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	83	100.0	172	1	PR39_PIG	P80054 sus scrofa
2	66	79.5	190	1	BCT7_BOVIN	P19661 bos taurus
3	59	71.1	166	2	Q6VY72	Q6VY72 bacterioph
4	58	69.9	164	2	P79361	P79361 ovis aries
5	58	69.9	190	1	BCT7_SHEEP	P50415 ovis aries
6	58	69.9	190	2	Q9XSQ9	Q9XSQ9 capra hircu
7	58	69.9	224	2	O19031	O19031 ovis aries
8	57	68.7	200	2	Q9RK54	Q9RK54 streptomyc
9	57	68.7	361	2	Q9XCG4	Q9XCG4 mycobacteri
10	55	66.3	337	2	Q7FLE7	Q7FLE7 oryza sativ
11	54	65.1	336	2	Q68405	Q68405 human cytom
12	53.5	64.5	397	2	Q7XTY0	Q7XTY0 oryza sativ
13	53	63.9	184	2	Q23291	Q23291 caenorhabdi
14	53	63.9	273	2	Q82PZ6	Q82PZ6 streptomyc
15	53	63.9	381	1	PRLP_BOVIN	Q9GKN8 bos taurus
16	52.5	63.3	82	1	COTT_BACSU	P11863 bacillus su
17	52	62.7	421	2	Q84R86	Q84R86 oryza sativ
18	52	62.7	1006	2	Q9LMQ1	Q9LMQ1 arabidopsis
19	51.5	62.0	159	2	Q656G1	Q656G1 oryza sativ
20	51.5	62.0	472	2	Q8C3A1	Q8C3A1 mus musculu
21	51.5	62.0	876	2	Q8CE88	Q8CE88 mus musculu
22	51.5	62.0	957	2	Q8CAV9	Q8CAV9 mus musculu
23	51.5	62.0	1187	1	PTNE_HUMAN	Q15678 homo sapien
24	51.5	62.0	1189	1	PTNE_MOUSE	Q62130 mus musculu
25	51	61.4	156	2	Q8RVJ2	Q8RVJ2 oryza sativ
26	51	61.4	194	2	Q6Z0W1	Q6Z0W1 oryza sativ
27	51	61.4	393	2	Q7QAH2	Q7QAH2 anopheles g
28	51	61.4	1729	2	Q8LLZ0	Q8LLZ0 oryza sativ
29	51	61.4	1729	2	Q7XGP6	Q7XGP6 oryza sativ
30	50.5	60.8	183	2	Q94J98	Q94J98 oryza sativ
31	50.5	60.8	432	2	Q96HM7	Q96HM7 homo sapien

32	50.5	60.8	1095	1	AT17_HUMAN	Q8te56 homo sapien
33	50	60.2	144	2	Q8LNW3	Q8lnw3 oryza sativ
34	50	60.2	192	2	P74661	P74661 synechocyst
35	50	60.2	206	2	Q8PHZ0	Q8phz0 xanthomonas
36	50	60.2	344	2	Q69260	Q69260 bovine herp
37	50	60.2	380	2	Q7Z727	Q7z727 homo sapien
38	50	60.2	384	2	Q6JAF9	Q6jaf9 sorghum bic
39	49.5	59.6	168	1	AP14_APIME	Q05601 apis mellif
40	49.5	59.6	177	2	Q9FSP4	Q9fsp4 oryza sativ
41	49.5	59.6	451	2	Q6EQW6	Q6eqw6 oryza sativ
42	49.5	59.6	602	2	Q66852	Q66852 avian adeno
43	49	59.0	195	2	Q96GV2	Q96gv2 homo sapien
44	49	59.0	210	2	Q9GZE0	Q9gze0 caenorhabdi
45	49	59.0	212	2	O08306	O08306 nocardioide

ALIGNMENTS

RESULT 1

ID	PR39_PIG	STANDARD;	PRT;	172 AA.
AC	P80054; Q9TR84;			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Antibacterial protein PR-39 precursor.			
GN	Name=PR39;			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95350216; PubMed=7624374;			
RA	Gudmundsson G.H.; Magnusson K.P.; Chowdhary B.P.; Johansson M.,			
RA	Andersson L.; Boman H.G.;			
RT	"Structure of the gene for porcine peptide antibiotic PR-39, a			
RT	cathelin gene family member; comparative mapping of the locus for the			
RT	human peptide antibiotic FALL-39.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=94071853; PubMed=8250863;			
RA	Storici P.; Zanetti M.;			
RT	"A cDNA derived from pig bone marrow cells predicts a sequence			
RT	identical to the intestinal antibacterial peptide PR-39.";			
RL	Biochem. Biophys. Res. Commun. 196:1058-1065(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;			
RA	Zhao C.; Ganz T.; Lehrer R.I.;			
RT	"Structures of genes for two cathelin-associated antimicrobial			
RT	peptides: prophenin-2 and PR-39.";			
RL	FEBS Lett. 376:130-134(1995).			
RN	[4]			
RP	SEQUENCE OF 131-169.			
RC	TISSUE=Intestine;			
RX	MEDLINE=92111534; PubMed=1765098;			
RA	Agerberth B.; Lee J.-Y.; Bergman T.; Carlquist M.; Boman H.G.,			
RA	Mutt V.; Joernvall H.;			
RT	"Amino acid sequence of PR-39. Isolation from pig intestine of a new			
RT	member of the family of proline-arginine-rich antibacterial			
RT	peptides.";			
RL	Eur. J. Biochem. 202:849-854(1991).			
RN	[5]			
RP	SEQUENCE OF 131-164, AND FUNCTION.			
RC	TISSUE=Neutrophils;			
RX	MEDLINE=95088504; PubMed=7996056;			
RA	Shi J.; Ross C.R.; Chengappa M.M.; Blecha F.;			
RT	"Identification of a proline-arginine-rich antibacterial peptide from			

RT neutrophils that is analogous to PR-39, an antibacterial peptide from  
RT the small intestine.";  
RL J. Leukoc. Biol. 56:807-811(1994).  
CC -1- FUNCTION: Exerts a potent antimicrobial activity against both  
CC E.coli and B.megaterium.  
CC -1- TISSUE SPECIFICITY: Small intestine and bone marrow.  
CC -1- SIMILARITY: Belongs to the cathelicidin family.  
CC -----  
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DR EMBL; X87236; CAA60682.1; -.  
DR EMBL; L23825; AAA31109.1; -.  
DR EMBL; X89201; CAA61487.1; -.  
DR PIR; S68232; S68232.  
DR HSSP; P32196; 1KWI.  
DR InterPro; IPR001894; Cathelicidin.  
DR Pfam; PF00666; Cathelicidins; 1.  
DR ProDom; PD001838; Cathelicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
DR Amidation; Antibiotic; Direct protein sequencing;  
KW Pyrrolidone carboxylic acid; Signal.  
FT SIGNAL 1 29 Potential.  
FT PROPEP 30 130  
FT CHAIN 131 169  
FT MOD\_RES 30 30  
FT -----  
FT Antibacterial protein PR-39.  
FT Pyrrolidone carboxylic acid (By  
FT similarity).  
FT By similarity.  
FT By similarity.  
FT Proline amide (G-170 provides amide  
FT group).  
FT G -> A (in Ref. 2).  
FT A -> T (in Ref. 1).  
FT RQ -> QR (in Ref. 1).  
FT IHS -> NDP (in Ref. 1).  
FT CONFLICT 117 119  
FT CONFLICT 157 157  
FT P -> I (in Ref. 5).  
SQ SEQUENCE 172 AA; 19476 MW; 994B792798C0E133 CRC64;

Query Match 100.0%; Score 83; DB 1; Length 172;  
Best Local Similarity 100.0%; Pred. No. 0.004;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRLPRP 14  
Db 131 RRRPRPPYLPRLPRP 144  
|||||

RESULT 2  
BCT7\_BOVIN STANDARD; PRT; 190 AA.  
AC P19661;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bactenecin 7 precursor (BAC7) (PR-59).  
GN Name=BAC7;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=95010707; PubMed=7925973; DOI=10.1016/0014-5793(94)00954-6;  
RA Scocchi M., Romeo D., Zanetti M.;  
RT "Molecular cloning of Bac7, a proline- and arginine-rich antimicrobial

peptide from bovine neutrophils.";  
FEBS Lett. 352:197-200(1994).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Scocchi M., Wang S., Zanetti M.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE OF 131-189, AND MASS SPECTROMETRY.  
RC TISSUE=Neutrophils;  
RX MEDLINE=91035404; PubMed=2229048;  
RA Frank R.W., Gennaro R., Schneider K., Przybylski M., Romeo D.;  
RT "Amino acid sequences of two proline-rich bactenecins. Antimicrobial  
peptides of bovine neutrophils.";  
RL J. Biol. Chem. 265:18871-18874(1990).  
[4]  
RP CHARACTERIZATION, AND MASS SPECTROMETRY.  
RX MEDLINE=96300243; PubMed=8706679;  
RA Storici P., Tossi A., Lenarcic B., Romeo D.;  
RT "Purification and structural characterization of bovine cathelicidins,  
precursors of antimicrobial peptides.";  
RL Eur. J. Biochem. 238:769-776(1996).  
CC -1- FUNCTION: Exerts, in vitro, a potent antimicrobial activity.  
CC Probably due to an impairment of the function of the respiratory  
chain and of energy-dependent activities in the inner membrane of  
susceptible microorganisms.  
CC -1- TISSUE SPECIFICITY: Large granules of neutrophils.  
CC -1- PTM: Elastase is responsible for its maturation.  
CC -1- MASS SPECTROMETRY: MW=18395; MW\_ERR=1; METHOD=Electrospray;  
CC RANGE=30-190; NOTE=Ref.4.  
CC -1- SIMILARITY: Belongs to the cathelicidin family.  
CC -----  
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CC -----

DR EMBL; L42977; AAA87359.1; -.  
DR EMBL; Y09471; CAA70616.1; -.  
DR HSSP; P32196; 1KWI.  
DR InterPro; IPR001894; Cathelicidin.  
DR Pfam; PF00666; Cathelicidins; 1.  
DR ProDom; PD001838; Cathelicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
KW Antibiotic; Direct protein sequencing; Pyrrolidone carboxylic acid;  
KW Repeat; Signal.

FT SIGNAL 1 29 Potential.  
FT PROPEP 30 130  
FT PEPTIDE 131 190 Bactenecin 7.  
FT PROPEP 189 190 Removed partially.  
FT MOD\_RES 30 30 Pyrrolidone carboxylic acid.  
FT DISULFID 85 96  
FT DISULFID 107 124  
SQ SEQUENCE 190 AA; 21567 MW; 8CD07D7AA30A731C CRC64;  
Query Match 79.5%; Score 66; DB 1; Length 190;  
Best Local Similarity 85.7%; Pred. No. 0.62;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRLPRP 14  
Db 132 RIRPRPRLPRRP 145  
|||||

RESULT 3  
Q6VY72 PRELIMINARY; PRT; 166 AA.  
ID Q6VY72  
AC Q6VY72;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Bacteriophage VWB.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC Lambda-like viruses.  
OX NCBI\_TaxID=10702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91037942; PubMed=2230721;  
RA Anne J., Van Mellaert L., Decock B., Van Damme J., Van Aerschot A.,  
RA Herdewijn P., Eyssen H.;  
RT "Further biological and molecular characterization of actinophage  
RT VWB.";  
RL J. Gen. Microbiol. 136:1365-1372(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95336309; PubMed=7611876;  
RA Anne J., Piten P., Van Mellaert L., Joris B., Opdenakker G.,  
RA Eyssen H.;  
RT "Analysis of the open reading frames of the main capsid proteins of  
RT actinophage VWB.";  
RL Arch. Virol. 140:1033-1047(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99098696; PubMed=9884227;  
RA Van Mellaert L., Mei L., Lammertyn E., Schacht S., Anne J.;  
RA "Site-specific integration of bacteriophage VWB genome into  
RT Streptomyces venezuelae and construction of a VWB-based integrative  
RT vector.";  
RL Microbiology 144:3351-3358(1998).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Van Dessel W., Van Mellaert L., Raasch C., Liesegang H., Streit W.,  
RA Anne J.;  
RT "Nucleotide sequence analysis of Streptomyces venezuelae bacteriophage  
RT VWB.";  
RL (In) Unknown A. (eds.);  
RL MICROBIAL IMMUNE EVASION STRATEGIES - MEETING OF THE BELGIAN SOCIETY  
RL FOR MICROBIOLOGY, pp.30-30, Unknown publisher (2003).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Anne J.F.C.;  
RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Van Mellaert L.M.G.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Van Dessel W., Van Mellaert L., Raasch C., Liesegang H., Streit W.,  
RA Anne J.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY320035; AAR29707.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 166 AA; 18526 MW; 7FA9BE7F95888A9B CRC64;

Query Match 71.1%; Score 59; DB 2; Length 166;  
Best Local Similarity 66.7%; Pred. No. 4.1;  
Matches 12; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 RRRPRPP- - - - YLPRPRP 14  
||||| : |||||  
Db 45 RRRPRPPFPSPHPRPRP 62

RESULT 4  
ID P79361 PRELIMINARY; PRT; 164 AA.  
AC P79361;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE 7.5 kDa bactinecin (Fragment).  
GN Name=Bac7.5;  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RX MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;  
RA Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.;  
RT "Molecular analysis of the sheep cathelin family reveals a novel  
RT antimicrobial peptide.";  
RL FEBS Lett. 377:519-522(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RA Huttner K.M., Mahoney M.M.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U60598; AAB49713.1; -.  
DR HSP; P32196; 1KWI.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
DR InterPro; IPR001894; Cathelicidin.  
DR Pfam; PF00666; Cathelicidins; 1.  
DR ProDom; PD001838; Cathelicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
FT NON TER 164  
SQ SEQUENCE 164 AA; 18642 MW; E3BFC871F6AE8B9A CRC64;

Query Match 69.9%; Score 58; DB 2; Length 164;  
Best Local Similarity 78.6%; Pred. No. 5.3;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRP 14  
||||| : |||||  
Db 132 RLRPRRRLPRPRP 145

RESULT 5  
BCT7\_SHEEP  
ID BCT7\_SHEEP STANDARD; PRT; 190 AA.  
AC P50415;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bactenecin 7 precursor (BAC7).  
GN Name=BAC7.5;  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Bone marrow;  
RX MEDLINE=96105386; PubMed=7498547; DOI=10.1016/0014-5793(95)01285-3;  
RA Bagella L., Scocchi M., Zanetti M.;  
RT "cDNA sequences of three sheep myeloid cathelicidins.";  
RL FEBS Lett. 376:225-228(1995).  
CC -!- FUNCTION: Exerts, in vitro, a potent antimicrobial activity.  
CC Probably due to an impairment of the function of the respiratory  
CC chain and of energy-dependent activities in the inner membrane of  
CC susceptible microorganisms (By similarity).  
CC -!- SIMILARITY: Belongs to the cathelicidin family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; L46852; AAA85468.1; -.  
DR PIR; S68230; S68230.  
DR HSSP; P32196; 1KWI.  
DR InterPro; IPR001894; Cathellicidin.  
DR Pfam; PF00666; Cathellicidins; 1.  
DR ProDom; PD001838; Cathellicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
KW Antibiotic; Pyrrolidone carboxylic acid; Repeat; Signal.  
FT SIGNAL 1 29 Potential.  
FT PROPEP 30 130 By similarity.  
FT CHAIN 131 190 Bactenecin 7.  
FT MOD\_RES 30 30 Pyrrolidone carboxylic acid (By  
FT similarity).  
FT DISULFID 85 96 By similarity.  
FT DISULFID 107 124 By similarity.  
SQ SEQUENCE 190 AA; 21829 MW; E4AAFBI600E98371 CRC64;

Query Match 69.9%; Score 58; DB 1; Length 190;  
Best Local Similarity 78.6%; Pred. No. 6.2;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRP 14  
| ||| | |||||  
Db 132 RLRPRRRLPRPRP 145

RESULT 6

Q9XSQ9 PRELIMINARY; PRT; 190 AA.  
AC Q9XSQ9;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Bac7.5 protein.  
GN Name=bac7.5;  
OS Capra hircus (Goat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Caprinae; Capra.  
OX NCBI\_TaxID=9925;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Bone marrow;  
RA Zhao C., Nguyen T., Brogden K., Lehrer R.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ243125; CAB45523.1; -.  
DR HSSP; P32196; 1KWI.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
DR InterPro; IPR001894; Cathellicidin.  
DR Pfam; PF00666; Cathellicidins; 1.  
DR ProDom; PD001838; Cathellicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
FT CHAIN 131 190 Bac7.5 protein.  
SQ SEQUENCE 190 AA; 21835 MW; D13305EF16875F4F CRC64;

Query Match 69.9%; Score 58; DB 2; Length 190;  
Best Local Similarity 78.6%; Pred. No. 6.2;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRP 14  
| ||| | |||||  
Db 132 RLRPRRRLPRPRP 145

RESULT 7

Q19031 PRELIMINARY; PRT; 224 AA.  
AC Q19031;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Bactinecin 11.  
GN Name=Bac11;  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huttner K.M., Mahoney M.M.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U77049; AAB62000.1; -.  
DR EMBL; U77046; AAB62000.1; JOINED.  
DR EMBL; U77047; AAB62000.1; JOINED.  
DR EMBL; U77048; AAB62000.1; JOINED.  
DR HSSP; P32196; 1KWI.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.  
DR InterPro; IPR001894; Cathellicidin.  
DR Pfam; PF00666; Cathellicidins; 1.  
DR ProDom; PD001838; Cathellicidin; 1.  
DR PROSITE; PS00946; CATHELICIDINS\_1; 1.  
DR PROSITE; PS00947; CATHELICIDINS\_2; 1.  
SQ SEQUENCE 224 AA; 25669 MW; 6AAAB1256AC76FC CRC64;

Query Match 69.9%; Score 58; DB 2; Length 224;  
Best Local Similarity 78.6%; Pred. No. 7.4;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPRP 14  
| ||| | |||||  
Db 132 RLRPRRRLPRPRP 145

RESULT 8

Q9RK54 PRELIMINARY; PRT; 200 AA.  
AC Q9RK54;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein SCO0323.  
GN ORFNames=SCF12.02c;  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RT coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL; AL939105; CAB56128.1; -.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 200 AA; 22076 MW; 0DCBBEC5585803B5 CRC64;



Query Match 68.7%; Score 57; DB 2; Length 200;  
Best Local Similarity 76.9%; Pred. No. 8.8;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 13  
DB 118 RRHPEPPALPRRP 130

RESULT 9  
Q9XCG4 ID Q9XCG4 PRELIMINARY; PRT; 361 AA.  
AC Q9XCG4;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Mycobacterium avium.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1764;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2151;  
RX MEDLINE=22885473; PubMed=14523113; DOI=10.1099/mic.0.26528-0;  
RA Eckstein T.M., Belisle J.T., Inamine J.M.;  
RT "Proposed pathway for the biosynthesis of serovar-specific glycopeptidolipids in Mycobacterium avium serovar 2.";  
RL Microbiology 149:2797-2807(2003).  
DR EMBL; AF143772; AAD44199.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 361 AA; 40208 MW; AD01DBE825C1C9EA CRC64;

Query Match 68.7%; Score 57; DB 2; Length 361;  
Best Local Similarity 71.4%; Pred. No. 16;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
DB 32 RRRPRPPAAPHPPP 45

RESULT 10  
Q7F1E7 ID Q7F1E7 PRELIMINARY; PRT; 337 AA.  
AC Q7F1E7;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Putative amino acid permease.  
GN Name=OJ1191 A10.117;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP003888; BAD11568.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR InterPro; IPR002293; AA/rel\_permease1.  
KW Transmembrane.  
SQ SEQUENCE 337 AA; 36544 MW; 4053C3635F9CF6CC CRC64;

Query Match 66.3%; Score 55; DB 2; Length 337;  
Best Local Similarity 76.9%; Pred. No. 27;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRPRPPYLPRRP 14  
DB 320 RRRPRPPALPPPPP 332

RESULT 11  
Q68405 ID Q68405 PRELIMINARY; PRT; 336 AA.  
AC Q68405;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Orf UL151.  
OS Human cytomegalovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Cytomegalovirus.  
OX NCBI\_TaxID=10359;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Toledo;  
RX MEDLINE=96099416; PubMed=8523595;  
RA Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;  
RT "Human cytomegalovirus clinical isolates carry at least 19 genes not found in laboratory strains.";  
RL J. Virol. 70:78-83(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Toledo;  
RA Cha T.-A.;  
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U33331; AAA85892.1; -.  
SQ SEQUENCE 336 AA; 35116 MW; 9F865E5019F69D0C CRC64;

Query Match 65.1%; Score 54; DB 2; Length 336;  
Best Local Similarity 76.9%; Pred. No. 36;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRPRPPYLPRRP 14  
DB 279 RRPPIPPILQRP 291

RESULT 12  
Q7XTY0 ID Q7XTY0 PRELIMINARY; PRT; 397 AA.  
AC Q7XTY0;  
DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE OSJNBa0019K04.17 protein.  
GN Name=OSJNBa0019K04.17;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12447439; DOI=10.1038/nature01183;  
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,  
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,  
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,  
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,  
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,  
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,  
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,  
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,  
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,  
RA Han B.;  
RT "Sequence and analysis of rice chromosome 4.";  
RL Nature 420:316-320(2002).  
DR EMBL; AL606640; CAD41670.3; -.  
DR Gramene; Q7XTY0; -.



SQ SEQUENCE 397 AA; 43737 MW; BAFc545CBFA4EB22 CRC64;  
Query Match 64.5%; Score 53.5; DB 2; Length 397;  
Best Local Similarity 84.6%; Pred. No. 50;  
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 2 RRRPPPYLPRPRP 14  
Db 24 RPPRPP-LPRPRP 35  
RESULT 13  
Q23291 PRELIMINARY; PRT; 184 AA.  
AC Q23291;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein ZC404.1.  
GN Name=ZC404.1; ORFNames=ZC404.1;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG WormBase Consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
RT investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Bentley D., Le T.T.;  
RT "The sequence of C. elegans cosmid ZC404.";  
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RG WormBase Consortium;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U55363; AAA97967.1; -.  
DR PIR; T29373; T29373.  
DR WormBase; WBGene00022601; ZC404.1.  
DR WormPeP; ZC404.1; CE07592.  
KW Hypothetical protein.  
SQ SEQUENCE 184 AA; 21649 MW; 6D64D09EA91308F9 CRC64;  
Query Match 63.9%; Score 53; DB 2; Length 184;  
Best Local Similarity 90.0%; Pred. No. 26;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 RPPPPYLP 12  
Db 26 RPKPYLP 35  
RESULT 14  
Q82PZ6 PRELIMINARY; PRT; 273 AA.  
AC Q82PZ6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=SAV725;

OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=33903;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680;  
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,  
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
RT "Genome sequence of an industrial microorganism Streptomyces  
RT avermitilis: deducing the ability of producing secondary  
RT metabolites.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680;  
RX MEDLINE=22608306; PubMed=12692562;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  
RA Sakaki Y., Hattori M., Omura S.;  
RT "Complete genome sequence and comparative analysis of the industrial  
RT microorganism Streptomyces avermitilis.";  
RL Nat. Biotechnol. 21:526-531(2003).  
DR EMBL; AP005023; BAC68435.1; -.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 273 AA; 29246 MW; FE024904356085C1 CRC64;  
Query Match 63.9%; Score 53; DB 2; Length 273;  
Best Local Similarity 71.4%; Pred. No. 39;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 RRRPPPYLP 14  
Db 224 RRRPPPARPGSRP 237  
RESULT 15  
PRLP\_BOVIN STANDARD; PRT; 381 AA.  
ID PRLP\_BOVIN  
AC Q9GKN8;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Prolargin precursor (Proline-arginine-rich end leucine-rich repeat  
DE protein).  
GN Name=PRELP;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Articular cartilage;  
RX MEDLINE=20576219; PubMed=11007795; DOI=10.1074/jbc.M007917200;  
RA Bengtsson E., Asberg A., Heinegaard D., Sommarin Y., Spillmann D.;  
RT "The amino-terminal part of PRELP binds to heparin and heparan  
RT sulfate.";  
RL J. Biol. Chem. 275:40695-40702(2000).  
RN [2]  
RP FUNCTION.  
RX MEDLINE=21964083; PubMed=11847210; DOI=10.1074/jbc.M108285200;  
RA Bengtsson E., Moergelin M., Sasaki T., Timpl R., Heinegaard D.,  
RA Aspegberg A.;  
RT "The leucine-rich repeat protein PRELP binds perlecan and collagens  
RT and may function as a basement membrane anchor.";  
RL J. Biol. Chem. 277:15061-15068(2002).  
CC -!- FUNCTION: May anchor basement membranes to the underlying  
CC connective tissue.  
CC -!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan  
CC perlecan and triple helical collagens type I and type II.  
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.

CC -!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and  
CC heparan sulfate. Binds collagens type I and type II through its  
CC leucine-rich repeat domain.  
CC -!- SIMILARITY: Belongs to the small leucine-rich proteoglycan (SLRP)  
CC family. Class II subfamily.  
CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF163568; AAG23723.1; -.  
DR HSSP; P25146; 106S.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003591; LRR\_typ.  
DR Pfam; PF00560; LRR; 11.  
DR Pfam; PF01462; LRRNT; 1.  
DR PRINTS; PR00019; LEURICHRPT.  
DR SMART; SM00013; LRRNT; 1.  
DR Extracellular matrix; Glycoprotein; Leucine-rich repeat; Repeat;  
KW Signal.  
FT SIGNAL 1 21 Potential.  
FT CHAIN 22 381 Prolargin.  
FT DOMAIN 72 88 Cys-rich.  
FT REPEAT 94 113 LRR-S 1.  
FT REPEAT 114 137 LRR-T 1.  
FT REPEAT 138 161 LRR-T 2.  
FT REPEAT 162 182 LRR-S 2.  
FT REPEAT 183 206 LRR-T 3.  
FT REPEAT 207 232 LRR-T 4.  
FT REPEAT 233 253 LRR-S 3.  
FT REPEAT 254 277 LRR-T 5.  
FT REPEAT 278 302 LRR-T 6.  
FT REPEAT 303 322 LRR-S 4.  
FT REPEAT 323 361 LRR-T 7.  
FT REPEAT 362 381 LRR-T 8.  
FT DOMAIN 196 201 Poly-Leu.  
FT DISULFID 331 372 By similarity.  
FT CARBOHYD 123 123 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 288 288 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 319 319 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 326 326 N-linked (GlcNAc. . .) (Potential).  
SQ SEQUENCE 381 AA; 43682 MW; 23DA99C01BB772A0 CRC64;  
  
Query Match 63.9%; Score 53; DB 1; Length 381;  
Best Local Similarity 76.9%; Pred. No. 55;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 RRRPPVLP RRP 14  
Db 25 RRRPPVLP RRP 37

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:02:04 ; Search time 14.3818 Seconds  
(without alignments)  
72.667 Million cell updates/sec

Title: US-10-014-147-7  
Perfect score: 83  
Sequence: 1 RRRPRPPYLPRRP 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	14	3	US-09-024-975-4 Sequence 4, Appli
2	83	100.0	14	4	US-08-930-777A-7 Sequence 7, Appli
3	83	100.0	19	4	US-08-930-777A-4 Sequence 4, Appli
4	83	100.0	26	2	US-08-419-066-2 Sequence 2, Appli
5	83	100.0	26	3	US-09-024-975-2 Sequence 2, Appli
6	83	100.0	26	4	US-08-930-777A-2 Sequence 1, Appli
7	83	100.0	38	4	US-09-739-535-1 Sequence 1, Appli
8	83	100.0	39	1	US-08-162-052-1 Sequence 1, Appli
9	83	100.0	39	1	US-08-310-722-1 Sequence 1, Appli
10	83	100.0	39	2	US-08-419-066-1 Sequence 1, Appli
11	83	100.0	39	2	US-08-728-333-1 Sequence 1, Appli
12	83	100.0	39	3	US-09-024-975-1 Sequence 1, Appli
13	83	100.0	39	4	US-08-930-777A-1 Sequence 1, Appli
14	83	100.0	39	5	PCT-US95-12080-1 Sequence 1, Appli
15	68	81.9	23	4	US-08-930-777A-3 Sequence 3, Appli
16	66	79.5	20	3	US-09-024-975-9 Sequence 9, Appli
17	66	79.5	59	4	US-09-030-619-163 Sequence 163, App
18	59	71.1	59	5	PCT-US95-12080-3 Sequence 3, Appli
19	54	65.1	336	1	US-08-414-926A-26 Sequence 26, Appl
20	54	65.1	336	2	US-08-926-922-26 Sequence 26, Appl
21	54	65.1	336	3	US-09-253-682-26 Sequence 26, Appl
22	54	65.1	336	3	US-09-527-657-26 Sequence 26, Appl
23	54	65.1	336	4	US-09-892-100-26 Sequence 32578, A
24	54	65.1	594	4	US-09-252-991A-32578 Sequence 29050, A
25	51.5	62.0	381	4	US-09-252-991A-29050 Sequence 21389, A
26	51	61.4	159	4	US-09-252-991A-21389 Sequence 24767, A
27	51	61.4	642	4	US-09-252-991A-24767 Sequence 24767, A

28	51	61.4	955	4	US-09-252-991A-24254	Sequence 24254, A
29	50	60.2	193	4	US-09-252-991A-29164	Sequence 29164, A
30	50	60.2	879	4	US-09-252-991A-19784	Sequence 19784, A
31	49	59.0	26	3	US-09-024-975-8	Sequence 8, Appli
32	49	59.0	138	4	US-09-252-991A-32675	Sequence 32675, A
33	49	59.0	179	4	US-09-252-991A-24900	Sequence 24900, A
34	49	59.0	257	4	US-09-252-991A-31868	Sequence 31868, A
35	49	59.0	326	4	US-09-252-991A-18844	Sequence 18844, A
36	49	59.0	439	4	US-09-252-991A-31919	Sequence 31919, A
37	49	59.0	506	4	US-09-672-785-8	Sequence 8, Appli
38	48	57.8	93	4	US-09-252-991A-29133	Sequence 29133, A
39	48	57.8	172	4	US-09-252-991A-26133	Sequence 26133, A
40	48	57.8	249	4	US-09-252-991A-21188	Sequence 21188, A
41	48	57.8	262	4	US-09-902-540-12987	Sequence 12987, A
42	48	57.8	280	4	US-09-252-991A-17338	Sequence 17338, A
43	48	57.8	311	4	US-09-252-991A-22406	Sequence 22406, A
44	48	57.8	366	6	5470718-4	Patent No. 5470718
45	48	57.8	366	6	5470718-4	Patent No. 5470718

ALIGNMENTS

RESULT 1  
US-09-024-975-4  
; Sequence 4, Application US/09024975  
; Patent No. 6133233  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, CHRISTOPHER R.  
; APPLICANT: BLECHA, FRANK  
; APPLICANT: SHI, JISHU  
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
; STREET: 2405 GRAND BLVD., SUITE 400  
; CITY: KANSAS CITY  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/024,975  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/802,306  
; APPLICATION NUMBER: 18-FEB-1997  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COLLINS, JOHN M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 25585-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 816/474-9050  
; TELEFAX: 816/474-9057  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-024-975-4

Query Match 100.0%; Score 83; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RRRPRPPYLPRRP 14  
|||||

Db 1 RRRPRPPYLPRRP 14

RESULT 2

US-08-930-777A-7

; Sequence 7, Application US/08930777A

; Patent No. 6713605

; GENERAL INFORMATION:

; APPLICANT: Blecha, Frank

; APPLICANT: Shi, Jishu

; TITLE OF INVENTION: Synthetic Antimicrobial Peptide

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hovey, Williams, Timmons & Collins

; STREET: 2405 Grand Blvd., Ste. 400

; CITY: Kansas City

; STATE: Missouri

; COUNTRY: U.S.A.

; ZIP: 64108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/930,777A

; FILING DATE: October 8, 1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/04674

; FILING DATE: April 10, 1996

; TELEPHONE: (816) 474-9050

; TELEFAX: (816) 474-9057

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-930-777A-7

Query Match 100.0%; Score 83; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14

Db 1 RRRPRPPYLPRRP 14

RESULT 3

US-08-930-777A-4

; Sequence 4, Application US/08930777A

; Patent No. 6713605

; GENERAL INFORMATION:

; APPLICANT: Blecha, Frank

; APPLICANT: Shi, Jishu

; TITLE OF INVENTION: Synthetic Antimicrobial Peptide

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hovey, Williams, Timmons & Collins

; STREET: 2405 Grand Blvd., Ste. 400

; CITY: Kansas City

; STATE: Missouri

; COUNTRY: U.S.A.

; ZIP: 64108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/930,777A

; FILING DATE: October 8, 1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/04674

; FILING DATE: April 10, 1996

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Collins, John M.

; REGISTRATION NUMBER: 26,262

; REFERENCE/DOCKET NUMBER: 23625-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (816) 474-9050

; TELEFAX: (816) 474-9057

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-930-777A-4

Query Match 100.0%; Score 83; DB 4; Length 19;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14

Db 1 RRRPRPPYLPRRP 14

RESULT 4

US-08-419-066-2

; Sequence 2, Application US/08419066

; Patent No. 5830993

; GENERAL INFORMATION:

; APPLICANT: Blecha, Frank

; APPLICANT: Shi, Jishu

; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &

; ADDRESSEE: Collins

; STREET: 2405 Grand Boulevard, Suite 400

; CITY: Kansas City

; STATE: Missouri

; COUNTRY: U.S.A.

; ZIP: 64108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/419,066

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Collins, John M.

; REGISTRATION NUMBER: 26262

; REFERENCE/DOCKET NUMBER: 23625

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (816) 474-9050

; TELEFAX: (816) 474-9057

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 amino acids

; TYPE: amino acid



STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-419-066-2

Query Match 100.0%; Score 83; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00031;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RRP 14  
Db 1 RRRPPPPYLP RRP 14

RESULT 5  
US-09-024-975-2  
; Sequence 2, Application US/09024975  
; Patent No. 6133233  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, CHRISTOPHER R.  
; APPLICANT: BLECHA, FRANK  
; APPLICANT: SHI, JISHU  
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
; STREET: 2405 GRAND BLVD., SUITE 400  
; CITY: KANSAS CITY  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/024,975  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/802,306  
; FILING DATE: 18-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COLLINS, JOHN M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 25585-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 816/474-9050  
; TELEFAX: 816/474-9057  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-024-975-2

Query Match 100.0%; Score 83; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00031;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RRP 14  
Db 1 RRRPPPPYLP RRP 14

RESULT 6  
US-08-930-777A-2  
; Sequence 2, Application US/08930777A

Patent No. 6713605  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-930-777A-2

Query Match 100.0%; Score 83; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00031;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RRP 14  
Db 1 RRRPPPPYLP RRP 14

RESULT 7  
US-09-739-535-1  
; Sequence 1, Application US/09739535  
; Patent No. 6794490  
; GENERAL INFORMATION:  
; APPLICANT: Cubist Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS  
; FILE REFERENCE: C060  
; CURRENT APPLICATION NUMBER: US/09/739,535  
; CURRENT FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-739-535-1

Query Match 100.0%; Score 83; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.00045;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RRRPRPPYLP RRP 14
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Db      1 RRRPRPPYLP RRP 14

RESULT 8
US-08-162-052-1
; Sequence 1, Application US/08162052
; Patent No. 5489575
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong-Youn
; APPLICANT: BOMAN, Hans G
; APPLICANT: MUTT, Viktor
; APPLICANT: JORNVAL, Hans
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,052
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9101838-2
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92-22578
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 003300-299
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-162-052-1

Query Match      100.0%; Score 83; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRPRPPYLP RRP 14
      |||||
Db      1 RRRPRPPYLP RRP 14

RESULT 9
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Mutt, Viktor
; AUTHORS: Jorrvall, Hans
; TITLE: No. 5654273el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-310-722-1

Query Match      100.0%; Score 83; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRPRPPYLP RRP 14
      |||||
Db      1 RRRPRPPYLP RRP 14

RESULT 10
US-08-419-066-1
; Sequence 1, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/419,066  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Collins, John M.  
;; REGISTRATION NUMBER: 26262  
;; REFERENCE/DOCKET NUMBER: 23625  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (816) 474-9050  
;; TELEFAX: (816) 474-9057  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 39 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
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US-08-419-066-1

\* Query Match 100.0%; Score 83; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
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Db 1 RRRPRPPYLPRRP 14

RESULT 11

US-08-728-333-1  
; Sequence 1, Application US/08728333  
; Patent No. 5863897  
; GENERAL INFORMATION:  
; APPLICANT: Gallo, Richard L.  
; APPLICANT: Klagsbrun, Michael  
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 1100 Peachtree Street, Suite 2800  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-4530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/728,333  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/310,722  
; FILING DATE: 22-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: CMCC379  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-815-6508  
; TELEFAX: (404)-815-6555  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

;;  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; PUBLICATION INFORMATION:  
;; AUTHORS: Lee, Jong-Youn  
;; AUTHORS: Boman, Hans G.  
;; AUTHORS: Mutt, Viktor  
;; AUTHORS: Jornvall, Hans  
;; TITLE: No. 5863897el Polypeptides And Their Use  
;; JOURNAL: PCT WO 92/22578  
;; DATE: 12/23/92  
;; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39  
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US-08-728-333-1

Query Match 100.0%; Score 83; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
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Db 1 RRRPRPPYLPRRP 14

RESULT 12

US-09-024-975-1  
; Sequence 1, Application US/09024975  
; Patent No. 6133233  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, CHRISTOPHER R.  
; APPLICANT: BLECHA, FRANK  
; APPLICANT: SHI, JISHU  
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
; STREET: 2405 GRAND BLVD., SUITE 400  
; CITY: KANSAS CITY  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
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; APPLICATION NUMBER: US/09/024,975  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/802,306  
; FILING DATE: 18-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COLLINS, JOHN M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 25585-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 816/474-9050  
; TELEFAX: 816/474-9057  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
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; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
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US-09-024-975-1

Query Match 100.0%; Score 83; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RRRPRPPYLPRRP 14

RESULT 13  
US-08-930-777A-1  
; Sequence 1, Application US/08930777A  
; Patent No. 6713605  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
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; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-930-777A-1

Query Match 100.0%; Score 83; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RRRPRPPYLPRRP 14

RESULT 14  
PCT-US95-12080-1  
; Sequence 1, Application PC/TUS9512080  
; GENERAL INFORMATION:  
; APPLICANT: Children's Medical Center Corporaton  
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/12080  
; FILING DATE:  
; CLASSIFICATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-873-8794  
; TELEFAX: (404)-815-8795  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; PUBLICATION INFORMATION:  
; AUTHORS: Lee, Jong-Youn  
; AUTHORS: Boman, Hans G.  
; AUTHORS: Mutt, Viktor  
; AUTHORS: Jornvall, Hans  
; TITLE: Novel Polypeptides And Their Use  
; JOURNAL: PCT WO 92/22578  
; DATE: 12/23/92  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39  
; PCT-US95-12080-1

Query Match 100.0%; Score 83; DB 5; Length 39;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRP 14  
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Db 1 RRRPRPPYLPRRP 14

RESULT 15  
US-08-930-777A-3  
; Sequence 3, Application US/08930777A  
; Patent No. 6713605  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; APPLICANT: Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-930-777A-3

Query Match 81.9%; Score 68; DB 4; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 PRPPYLPRPRP 11

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Job time : 15.3818 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:05:05 ; Search time 51.6727 Seconds  
(without alignments)  
113.119 Million cell updates/sec

Title: US-10-014-147-7

Perfect score: 83

Sequence: 1 RRRPRPPYLPRRP 14

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Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	14	14 US-10-014-147-7	Sequence 7, Appli
2	83	100.0	14	15 US-10-651-147-7	Sequence 7, Appli
3	83	100.0	15	15 US-10-391-155-3	Sequence 3, Appli
4	83	100.0	19	14 US-10-014-147-4	Sequence 4, Appli
5	83	100.0	19	15 US-10-651-147-4	Sequence 4, Appli
6	83	100.0	26	14 US-10-014-147-2	Sequence 2, Appli
7	83	100.0	26	15 US-10-651-147-2	Sequence 2, Appli
8	83	100.0	38	9 US-09-738-742-1	Sequence 1, Appli
9	83	100.0	38	9 US-09-739-535-1	Sequence 1, Appli
10	83	100.0	39	14 US-10-014-147-1	Sequence 1, Appli
11	83	100.0	39	15 US-10-391-155-1	Sequence 1, Appli

12	83	100.0	39	15 US-10-391-155-2	Sequence 2, Appli
13	83	100.0	39	15 US-10-391-155-6	Sequence 6, Appli
14	83	100.0	39	15 US-10-651-147-1	Sequence 1, Appli
15	83	100.0	42	16 US-10-344-709C-18	Sequence 18, Appli
16	83	100.0	42	17 US-10-916-185-14	Sequence 14, Appli
17	83	100.0	42	18 US-10-991-286A-44	Sequence 44, Appli
18	83	100.0	42	20 US-11-004-379-20	Sequence 20, Appli
19	68	81.9	23	14 US-10-014-147-3	Sequence 3, Appli
20	68	81.9	23	15 US-10-651-147-3	Sequence 3, Appli
21	66	79.5	59	9 US-09-030-619-163	Sequence 163, App
22	66	79.5	59	9 US-09-912-609-51	Sequence 51, Appli
23	66	79.5	59	15 US-10-277-232-163	Sequence 163, App
24	66	79.5	59	15 US-10-277-233-163	Sequence 163, App
25	66	79.5	59	17 US-10-838-289-683	Sequence 683, App
26	66	79.5	60	16 US-10-344-709C-17	Sequence 17, Appli
27	64	77.1	11	15 US-10-391-155-4	Sequence 4, Appli
28	64	77.1	11	18 US-10-502-639-1	Sequence 1, Appli
29	63.5	76.5	234	16 US-10-425-115-344157	Sequence 344157,
30	59	71.1	11	17 US-10-475-403-5	Sequence 5, Appli
31	58	69.9	109	16 US-10-767-701-54214	Sequence 54214, A
32	56	67.5	138	16 US-10-437-963-185069	Sequence 185069,
33	56	67.5	179	16 US-10-425-115-230007	Sequence 230007,
34	56	67.5	243	16 US-10-425-115-230009	Sequence 230009,
35	56	67.5	245	16 US-10-425-115-206869	Sequence 206869,
36	56	67.5	692	11 US-09-758-759-79	Sequence 79, Appli
37	55	66.3	45	9 US-09-864-761-49065	Sequence 49065, A
38	55	66.3	53	16 US-10-437-963-180460	Sequence 180460,
39	55	66.3	75	16 US-10-425-115-229056	Sequence 229056,
40	55	66.3	179	16 US-10-437-963-134743	Sequence 134743,
41	55	66.3	200	16 US-10-425-115-206766	Sequence 206766,
42	55	66.3	225	16 US-10-437-963-118568	Sequence 118568,
43	55	66.3	388	16 US-10-437-963-160033	Sequence 160033,
44	54	65.1	163	16 US-10-437-963-114067	Sequence 114067,
45	54	65.1	208	16 US-10-437-963-131115	Sequence 131115,

ALIGNMENTS

RESULT 1  
US-10-014-147-7  
; Sequence 7, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/014,147  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-014-147-7  
Query Match 100.0%; Score 83; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRP 14  
Db 1 RRRPRPPYLP RRP 14  
RESULT 2  
US-10-651-147-7  
Sequence 7, Application US/10651147  
Publication No. US20040043934A1  
GENERAL INFORMATION:  
APPLICANT: Blecha, Frank  
Shi, Jishu  
TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hovey, Williams, Timmons & Collins  
STREET: 2405 Grand Blvd., Ste. 400  
CITY: Kansas City  
STATE: Missouri  
COUNTRY: U.S.A.  
ZIP: 64108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/651,147  
FILING DATE: 28-Aug-2003  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/930,777A  
FILING DATE: October 8, 1997  
APPLICATION NUMBER: PCT/US96/04674  
FILING DATE: April 10, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Collins, John M.  
REGISTRATION NUMBER: 26,262  
REFERENCE/DOCKET NUMBER: 23625-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (816) 474-9050  
TELEFAX: (816) 474-9057  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-651-147-7  
Query Match 100.0%; Score 83; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRP 14  
Db 1 RRRPRPPYLP RRP 14

Db 1 RRRPRPPYLP RRP 14  
RESULT 3  
US-10-391-155-3  
Sequence 3, Application US/10391155  
Publication No. US20040009463A1  
GENERAL INFORMATION:  
APPLICANT: Simons, Michael  
Gao, Youhe  
TITLE OF INVENTION: Method for PR-39 peptide mediated  
selective inhibition of IKBA degradation  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David Prashker, Esq.  
STREET: P.O. Box 5387  
CITY: Magnolia  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 01930  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
COMPUTER: Dell PC  
OPERATING SYSTEM: MS XP  
SOFTWARE: WordPerfect version 10  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/391,155  
FILING DATE: 18-Mar-2003  
CLASSIFICATION: Unknown  
ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker, Esq.  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: BIS-044/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-391-155-3  
Query Match 100.0%; Score 83; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRP 14  
Db 1 RRRPRPPYLP RRP 14  
RESULT 4  
US-10-014-147-4  
Sequence 4, Application US/10014147  
Publication No. US20030125249A1  
GENERAL INFORMATION:  
APPLICANT: Blecha, Frank  
Shi, Jishu  
TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hovey, Williams, Timmons & Collins  
STREET: 2405 Grand Blvd., Ste. 400  
CITY: Kansas City  
STATE: Missouri  
COUNTRY: U.S.A.  
ZIP: 64108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/014,147  
;; FILING DATE: 07-Dec-2001  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/930,777A  
;; FILING DATE: October 8, 1997  
;; APPLICATION NUMBER: PCT/US96/04674  
;; FILING DATE: April 10, 1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Collins, John M.  
;; REGISTRATION NUMBER: 26,262  
;; REFERENCE/DOCKET NUMBER: 23625-A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (816) 474-9050  
;; TELEFAX: (816) 474-9057  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 19 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-014-147-4  
Query Match 100.0%; Score 83; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLP RPRP 14

RESULT 5  
US-10-651-147-4  
; Sequence 4, Application US/106511147  
; Publication No. US20040043934A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/651,147  
; FILING DATE: 28-Aug-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057

;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 19 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-651-147-4

Query Match 100.0%; Score 83; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLP RPRP 14

RESULT 6  
US-10-014-147-2  
; Sequence 2, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/014,147  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-014-147-2  
Query Match 100.0%; Score 83; DB 14; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.006;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLP RPRP 14

RESULT 7  
US-10-651-147-2  
; Sequence 2, Application US/10651147  
; Publication No. US20040043934A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/651,147  
; FILING DATE: 28-Aug-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262  
; REFERENCE/DOCKET NUMBER: 23625-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (816) 474-9050  
; TELEFAX: (816) 474-9057  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-651-147-2  
Query Match 100.0%; Score 83; DB 15; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.006;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLP RRP 14  
RESULT 8  
US-09-738-742-1  
; Sequence 1, Application US/09738742  
; Publication No. US20020025924A1  
; GENERAL INFORMATION:  
; APPLICANT: Cubist Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS  
; FILE REFERENCE: C060  
; CURRENT APPLICATION NUMBER: US/09/738,742  
; CURRENT FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic

US-09-738-742-1  
Query Match 100.0%; Score 83; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.0082;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLP RRP 14  
RESULT 9  
US-09-739-535-1  
; Sequence 1, Application US/09739535  
; Publication No. US20020058785A1  
; GENERAL INFORMATION:  
; APPLICANT: Cubist Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL LIPOPEPTIDES AS ANTIBACTERIAL AGENTS  
; FILE REFERENCE: C060  
; CURRENT APPLICATION NUMBER: US/09/739,535  
; CURRENT FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-739-535-1  
Query Match 100.0%; Score 83; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0.0082;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRPRPPYLP RRP 14  
| | | | | | | | | |  
Db 1 RRRPRPPYLP RRP 14  
RESULT 10  
US-10-014-147-1  
; Sequence 1, Application US/10014147  
; Publication No. US20030125249A1  
; GENERAL INFORMATION:  
; APPLICANT: Blecha, Frank  
; Shi, Jishu  
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hovey, Williams, Timmons & Collins  
; STREET: 2405 Grand Blvd., Ste. 400  
; CITY: Kansas City  
; STATE: Missouri  
; COUNTRY: U.S.A.  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/014,147  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,777A  
; FILING DATE: October 8, 1997  
; APPLICATION NUMBER: PCT/US96/04674  
; FILING DATE: April 10, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Collins, John M.  
; REGISTRATION NUMBER: 26,262



```

; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-014-147-1
Query Match 100.0%; Score 83; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14
Db 1 RRRPRPPYLP RPRP 14

RESULT 11
US-10-391-155-1
; Sequence 1, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-391-155-1
Query Match 100.0%; Score 83; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14
Db 1 RRRPRPPYLP RPRP 14

US-10-391-155-1
Query Match 100.0%; Score 83; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14
Db 1 RRRPRPPYLP RPRP 14
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RESULT 12
US-10-391-155-2
; Sequence 2, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-391-155-2
Query Match 100.0%; Score 83; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14
Db 1 RRRPRPPYLP RPRP 14

RESULT 13
US-10-391-155-6
; Sequence 6, Application US/10391155
; Publication No. US20040009463A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Gao, Youhe
; TITLE OF INVENTION: Method for PR-39 peptide mediated
; selective inhibition of IKBA degradation
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS XP
; SOFTWARE: WordPerfect version 10
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6
Query Match      100.0%; Score 83; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPRPPYLPRPRP 14
Db      1 RRRPRPPYLPRPRP 14

RESULT 14
US-10-651-147-1
; Sequence 1, Application US/10651147
; Publication No. US20040043934A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/651,147
; FILING DATE: 28-Aug-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/391,155
; FILING DATE: 18-Mar-2003
; CLASSIFICATION: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-044/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-391-155-6
Query Match      100.0%; Score 83; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPRPPYLPRPRP 14
Db      1 RRRPRPPYLPRPRP 14

RESULT 15
US-10-344-709C-18
; Sequence 18, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof
; FILE REFERENCE: SONN:030US
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-18
Query Match      100.0%; Score 83; DB 16; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRPRPPYLPRPRP 14
Db      1 RRRPRPPYLPRPRP 14

Search completed: October 26, 2005, 05:29:00
Job time : 53.6727 secs
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